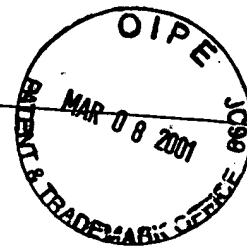


SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN DIJKE
- (ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING IT, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 46

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
(B) STREET: 666 Fifth Avenue
(C) CITY: New York City
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10103

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/039,177
(B) FILING DATE: March 13, 1998
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/GB93/02367
(B) FILING DATE: November 17, 1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: GB 9224057.1
(B) FILING DATE: November 17, 1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: GB 9304677.9
(B) FILING DATE: March 8, 1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: GB 9304680.3
(B) FILING DATE: March 8, 1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 9311047.6
(B) FILING DATE: May 28, 1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 9313763.6
(B) FILING DATE: July 2, 1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 9136099.2
(B) FILING DATE: August 3, 1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 321344.5

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(B) FILING DATE: October 15, 1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mary Anne Schofield
(B) REGISTRATION NUMBER: 36,669
(C) REFERENCE/DOCKET NUMBER: LUD 5539 CIP - JEL/MAS

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 662-0200
(B) TELEFAX: (202) 662-4643

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1984 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 283..1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCCCCGT      180
CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA      240
AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC      294
                               Met Thr Leu Gly
                               1
TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG      342
Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln
   5              10              15              20

GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT      390
Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys
          25              30              35

GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA      438
Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr
      40              45              50
```

GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly 55 60 65	486
TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe 70 75 80	534
GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser 85 90 95 100	582
CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp 105 110 115	630
GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu 120 125 130	678
GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu 135 140 145	726
AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu 150 155 160	774
AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser 165 170 175 180	822
GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg 185 190 195	870
ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg 200 205 210	918
TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val 215 220 225	966
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ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile 245 250 255 260	1062
GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG CTG TGG CTC ATC Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile 265 270 275	1110
ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln 280 285 290	1158

ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC	1206
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Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro	
310 315 320	
GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC	1302
Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser	
325 330 335 340	
AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA	1350
Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser	
345 350 355	
CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC	1398
Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr	
360 365 370	
AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC	1446
Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp	
375 380 385	
TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG	1494
Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val	
390 395 400	
CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC	1542
Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp	
405 410 415 420	
TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG	1590
Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu	
425 430 435	
GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT	1638
Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro	
440 445 450	
AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG	1686
Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met	
455 460 465	
CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG	1734
Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg	
470 475 480	
ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA	1782
Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys	
485 490 495 500	
GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC	1831
Val Ile Gln	
TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG	1891
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ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA	1984

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Leu	Val	Thr	Gln	Gly	Asp	Pro	Val	Lys	Pro	Ser	Arg	Gly	Pro	Leu	Val
			20					25					30		
Thr	Cys	Thr	Cys	Glu	Ser	Pro	His	Cys	Lys	Gly	Pro	Thr	Cys	Arg	Gly
			35				40					45			
Ala	Trp	Cys	Thr	Val	Val	Leu	Val	Arg	Glu	Glu	Gly	Arg	His	Pro	Gln
	50					55					60				
Glu	His	Arg	Gly	Cys	Gly	Asn	Leu	His	Arg	Glu	Leu	Cys	Arg	Gly	Arg
65					70					75					80
Pro	Thr	Glu	Phe	Val	Asn	His	Tyr	Cys	Cys	Asp	Ser	His	Leu	Cys	Asn
				85				90						95	
His	Asn	Val	Ser	Leu	Val	Leu	Glu	Ala	Thr	Gln	Pro	Pro	Ser	Glu	Gln
			100					105					110		
Pro	Gly	Thr	Asp	Gly	Gln	Leu	Ala	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala
		115				120						125			
Leu	Leu	Ala	Leu	Val	Ala	Leu	Gly	Val	Leu	Gly	Leu	Trp	His	Val	Arg
	130					135						140			
Arg	Arg	Gln	Glu	Lys	Gln	Arg	Gly	Leu	His	Ser	Glu	Leu	Gly	Glu	Ser
145					150					155					160
Ser	Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp
				165					170					175	
Leu	Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe
			180					185					190		
Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val
		195				200						205			
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu
	210				215						220				
Ser	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe
225					230					235					240
Arg	Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Arg	His	Asp	Asn	Ile	
				245					250				255		
Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln
			260					265					270		
Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe
		275					280						285		
Leu	Gln	Arg	Gln	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu	Arg	Leu	Ala	Val
	290					295					300				
Ser	Ala	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr
305					310					315					320
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Arg	Asn	Val
				325					330					335	
Leu	Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala
			340					345					350		
Val	Met	His	Ser	Gln	Gly	Ser	Asp	Tyr	Leu	Asp	Ile	Gly	Asn	Asn	Pro
		355					360					365			
Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Gln
	370					375						380			

Ile	Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala
385					390					395					400
Phe	Gly	Leu	Val	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Thr	Ile	Val	Asn	Gly
				405					410					415	
Ile	Val	Glu	Asp	Tyr	Arg	Pro	Pro	Phe	Tyr	Asp	Val	Val	Pro	Asn	Asp
			420					425					430		
Pro	Ser	Phe	Glu	Asp	Met	Lys	Lys	Val	Val	Cys	Val	Asp	Gln	Gln	Thr
		435				440						445			
Pro	Thr	Ile	Pro	Asn	Arg	Leu	Ala	Ala	Asp	Pro	Val	Leu	Ser	Gly	Leu
	450					455					460				
Ala	Gln	Met	Met	Arg	Glu	Cys	Trp	Tyr	Pro	Asn	Pro	Ser	Ala	Arg	Leu
465					470					475					480
Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Gln	Lys	Ile	Ser	Asn	Ser	Pro
			485						490					495	
Glu	Lys	Pro	Lys	Val	Ile	Gln									
			500												

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 104..1630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG CGGCTTGAAG	60
GACTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA	115
Met Val Asp Gly	
1	
GTG ATG ATT CTT CCT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT	163
Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser	
5 10 15 20	
ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG	211
Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val	
25 30 35	
TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG	259
Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln	
40 45 50	

TGC	TTT	TCC	TCA	CTG	AGC	ATC	AAC	GAT	GGC	TTC	CAC	GTC	TAC	CAG	AAA	307
Cys	Phe	Ser	Ser	Leu	Ser	Ile	Asn	Asp	Gly	Phe	His	Val	Tyr	Gln	Lys	
		55					60					65				
GGC	TGC	TTC	CAG	GTT	TAT	GAG	CAG	GGA	AAG	ATG	ACC	TGT	AAG	ACC	CCG	355
Gly	Cys	Phe	Gln	Val	Tyr	Glu	Gln	Gly	Lys	Met	Thr	Cys	Lys	Thr	Pro	
	70					75					80					
CCG	TCC	CCT	GGC	CAA	GCT	GTG	GAG	TGC	TGC	CAA	GGG	GAC	TGG	TGT	AAC	403
Pro	Ser	Pro	Gly	Gln	Ala	Val	Glu	Cys	Cys	Gln	Gly	Asp	Trp	Cys	Asn	
85					90					95					100	
AGG	AAC	ATC	ACG	GCC	CAG	CTG	CCC	ACT	AAA	GGA	AAA	TCC	TTC	CCT	GGA	451
Arg	Asn	Ile	Thr	Ala	Gln	Leu	Pro	Thr	Lys	Gly	Lys	Ser	Phe	Pro	Gly	
				105					110					115		
ACA	CAG	AAT	TTC	CAC	TTG	GAG	GTT	GGC	CTC	ATT	ATT	CTC	TCT	GTA	GTG	499
Thr	Gln	Asn	Phe	His	Leu	Glu	Val	Gly	Leu	Ile	Ile	Leu	Ser	Val	Val	
			120					125					130			
TTC	GCA	GTA	TGT	CTT	TTA	GCC	TGC	CTG	CTG	GGA	GTT	GCT	CTC	CGA	AAA	547
Phe	Ala	Val	Cys	Leu	Leu	Ala	Cys	Leu	Leu	Gly	Val	Ala	Leu	Arg	Lys	
		135					140					145				
TTT	AAA	AGG	CGC	AAC	CAA	GAA	CGC	CTC	AAT	CCC	CGA	GAC	GTG	GAG	TAT	595
Phe	Lys	Arg	Arg	Asn	Gln	Glu	Arg	Leu	Asn	Pro	Arg	Asp	Val	Glu	Tyr	
	150					155					160					
GGC	ACT	ATC	GAA	GGG	CTC	ATC	ACC	ACC	AAT	GTT	GGA	GAC	AGC	ACT	TTA	643
Gly	Thr	Ile	Glu	Gly	Leu	Ile	Thr	Thr	Asn	Val	Gly	Asp	Ser	Thr	Leu	
165					170					175					180	
GCA	GAT	TTA	TTG	GAT	CAT	TCG	TGT	ACA	TCA	GGA	AGT	GGC	TCT	GGT	CTT	691
Ala	Asp	Leu	Leu	Asp	His	Ser	Cys	Thr	Ser	Gly	Ser	Gly	Ser	Gly	Leu	
				185					190					195		
CCT	TTT	CTG	GTA	CAA	AGA	ACA	GTG	GCT	CGC	CAG	ATT	ACA	CTG	TTG	GAG	739
Pro	Phe	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Ile	Thr	Leu	Leu	Glu	
			200					205					210			
TGT	GTC	GGG	AAA	GGC	AGG	TAT	GGT	GAG	GTG	TGG	AGG	GGC	AGC	TGG	CAA	787
Cys	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Ser	Trp	Gln	
		215					220					225				
GGG	GAA	AAT	GTT	GCC	GTG	AAG	ATC	TTC	TCC	TCC	CGT	GAT	GAG	AAG	TCA	835
Gly	Glu	Asn	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Lys	Ser	
	230					235					240					
TGG	TTC	AGG	GAA	ACG	GAA	TTG	TAC	AAC	ACT	GTG	ATG	CTG	AGG	CAT	GAA	883
Trp	Phe	Arg	Glu	Thr	Glu	Leu	Tyr	Asn	Thr	Val	Met	Leu	Arg	His	Glu	
245					250					255					260	
AAT	ATC	TTA	GGT	TTC	ATT	GCT	TCA	GAC	ATG	ACA	TCA	AGA	CAC	TCC	AGT	931
Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	His	Ser	Ser	
				265					270					275		
ACC	CAG	CTG	TGG	TTA	ATT	ACA	CAT	TAT	CAT	GAA	ATG	GGA	TCG	TTG	TAC	979
Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	Met	Gly	Ser	Leu	Tyr	
			280					285					290			

GAC TAT CTT CAG CTT ACT ACT CTG GAT ACA GTT AGC TGC CTT CGA ATA	1027
Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser Cys Leu Arg Ile	
295 300 305	
GTG CTG TCC ATA GCT AGT GGT CTT GCA CAT TTG CAC ATA GAG ATA TTT	1075
Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Ile Glu Ile Phe	
310 315 320	
GGG ACC CAA GGG AAA CCA GCC ATT GCC CAT CGA GAT TTA AAG AGC AAA	1123
Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys	
325 330 335 340	
AAT ATT CTG GTT AAG AAG AAT GGA CAG TGT TGC ATA GCA GAT TTG GGC	1171
Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala Asp Leu Gly	
345 350 355	
CTG GCA GTC ATG CAT TCC CAG AGC ACC AAT CAG CTT GAT GTG GGG AAC	1219
Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp Val Gly Asn	
360 365 370	
AAT CCC CGT GTG GGC ACC AAG CGC TAC ATG GCC CCC GAA GTT CTA GAT	1267
Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp	
375 380 385	
GAA ACC ATC CAG GTG GAT TGT TTC GAT TCT TAT AAA AGG GTC GAT ATT	1315
Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg Val Asp Ile	
390 395 400	
TGG GCC TTT GGA CTT GTT TTG TGG GAA GTG GCC AGG CGG ATG GTG AGC	1363
Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg Met Val Ser	
405 410 415 420	
AAT GGT ATA GTG GAG GAT TAC AAG CCA CCG TTC TAC GAT GTG GTT CCC	1411
Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp Val Val Pro	
425 430 435	
AAT GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG GAT CAA	1459
Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln	
440 445 450	
CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC	1507
Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr	
455 460 465	
TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA	1555
Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala	
470 475 480	
AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT	1603
Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn	
485 490 495 500	
TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTC	1650
Ser Leu Asp Lys Leu Lys Thr Asp Cys	
505	
GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGGAC CTAATGCTGG CCTGACTGGT	1710
TGTCAGAATG GAATCCATCT GTCTCCCTCC CCAAATGGCT GCTTTGACAA GGCAGACGTC	1770

GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCACCCTA ACCTCGCTCG ATGACTGTGA	1830
ACTGGGCATT TCACGAACTG TTCACACTGC AGAGACTAAT GTTGGACAGA CACTGTTGCA	1890
AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGGCAT TAAGTCAGTG	1950
GCTTTGCATA GCTTTCACAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA AGGAGGTGGT	2010
GAATTTTAA TCAGCAATAT TGCCTGTGCT TCTCTTCTTT ATTGCACTAG GAATTCTTTG	2070
CATTCCTTAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTTGCCAA AATGTTGGCT	2130
GCGTACTCCA CTGGTCTGTC TTTGGATAAT AGGAATTCAA TTTGGCAAAA CAAAATGTAA	2190
TGTCAGACTT TGCTGCATTT TACACATGTG CTGATGTTTA CAATGATGCC GAACATTAGG	2250
AATTGTTTAT ACACAACTTT GCAAATTATT TATTACTTGT GCACTTAGTA GTTTTTACAA	2310
AACTGCTTTG TGCATATGTT AAAGCTTATT TTTATGTGGT CTTATGATTT TATTACAGAA	2370
ATGTTTTTAA CACTATACTC TAAAATGGAC ATTTTCTTTT ATTATCAGTT AAAATCACAT	2430
TTTAAGTGCT TCACATTTGT ATGTGTGTAG ACTGTAACCT TTTTTCAGTT CATATGCAGA	2490
ACGTATTTAG CCATTACCCA CGTGACACCA CCGAATATAT TATCGATTTA GAAGCAAAGA	2550
TTTCAGTAGA ATTTTAGTCC TGAACGCTAC GGGGAAAATG CATTTTCTTC AGAATTATCC	2610
ATTACGTGCA TTAAACTCT GCCAGAAAAA AATAACTATT TTGTTTTAAT CTACTTTTGT	2670
TATTTAGTAG TTATTTGTAT AAATTAAATA AACTGTTTTC AAGTCAAAAA AAAA	2724

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Val	Asp	Gly	Val	Met	Ile	Leu	Pro	Val	Leu	Ile	Met	Ile	Ala	Leu	1	5	10	15
Pro	Ser	Pro	Ser	Met	Glu	Asp	Glu	Lys	Pro	Lys	Val	Asn	Pro	Lys	Leu	20	25	30	
Tyr	Met	Cys	Val	Cys	Glu	Gly	Leu	Ser	Cys	Gly	Asn	Glu	Asp	His	Cys	35	40	45	
Glu	Gly	Gln	Gln	Cys	Phe	Ser	Leu	Ser	Ile	Asn	Asp	Gly	Phe	His		50	55	60	
Val	Tyr	Gln	Lys	Gly	Cys	Phe	Gln	Val	Tyr	Glu	Gln	Gly	Lys	Met	Thr	65	70	75	80
Cys	Lys	Thr	Pro	Pro	Ser	Pro	Gly	Gln	Ala	Val	Glu	Cys	Cys	Gln	Gly	85	90	95	
Asp	Trp	Cys	Asn	Arg	Asn	Ile	Thr	Ala	Gln	Leu	Pro	Thr	Lys	Gly	Lys	100	105	110	
Ser	Phe	Pro	Gly	Thr	Gln	Asn	Phe	His	Leu	Glu	Val	Gly	Leu	Ile	Ile	115	120	125	

Leu	Ser	Val	Val	Phe	Ala	Val	Cys	Leu	Leu	Ala	Cys	Leu	Leu	Gly	Val
130						135					140				
Ala	Leu	Arg	Lys	Phe	Lys	Arg	Arg	Asn	Gln	Glu	Arg	Leu	Asn	Pro	Arg
145					150					155					160
Asp	Val	Glu	Tyr	Gly	Thr	Ile	Glu	Gly	Leu	Ile	Thr	Thr	Asn	Val	Gly
				165					170					175	
Asp	Ser	Thr	Leu	Ala	Asp	Leu	Leu	Asp	His	Ser	Cys	Thr	Ser	Gly	Ser
			180					185					190		
Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Ile
		195					200					205			
Thr	Leu	Leu	Glu	Cys	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg
		210				215					220				
Gly	Ser	Trp	Gln	Gly	Glu	Asn	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg
225					230					235					240
Asp	Glu	Lys	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Leu	Tyr	Asn	Thr	Val	Met
			245						250					255	
Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser
			260					265					270		
Arg	His	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	Met
		275					280					285			
Gly	Ser	Leu	Tyr	Asp	Tyr	Leu	Gln	Leu	Thr	Thr	Leu	Asp	Thr	Val	Ser
		290				295					300				
Cys	Leu	Arg	Ile	Val	Leu	Ser	Ile	Ala	Ser	Gly	Leu	Ala	His	Leu	His
305					310					315					320
Ile	Glu	Ile	Phe	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp
			325						330					335	
Leu	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Gln	Cys	Cys	Ile
			340					345					350		
Ala	Asp	Leu	Gly	Leu	Ala	Val	Met	His	Ser	Gln	Ser	Thr	Asn	Gln	Leu
		355					360					365			
Asp	Val	Gly	Asn	Asn	Pro	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro
		370				375					380				
Glu	Val	Leu	Asp	Glu	Thr	Ile	Gln	Val	Asp	Cys	Phe	Asp	Ser	Tyr	Lys
385					390					395					400
Arg	Val	Asp	Ile	Trp	Ala	Phe	Gly	Leu	Val	Leu	Trp	Glu	Val	Ala	Arg
			405						410					415	
Arg	Met	Val	Ser	Asn	Gly	Ile	Val	Glu	Asp	Tyr	Lys	Pro	Pro	Phe	Tyr
			420					425					430		
Asp	Val	Val	Pro	Asn	Asp	Pro	Ser	Phe	Glu	Asp	Met	Arg	Lys	Val	Val
		435					440					445			
Cys	Val	Asp	Gln	Gln	Arg	Pro	Asn	Ile	Pro	Asn	Arg	Trp	Phe	Ser	Asp
		450				455					460				
Pro	Thr	Leu	Thr	Ser	Leu	Ala	Lys	Leu	Met	Lys	Glu	Cys	Trp	Tyr	Gln
465					470					475					480
Asn	Pro	Ser	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Thr
			485						490					495	
Lys	Ile	Asp	Asn	Ser	Leu	Asp	Lys	Leu	Lys	Thr	Asp	Cys			
			500					505							

- (2) INFORMATION FOR SEQ ID NO: 5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2932 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 310..1905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA AAATATGCAT	60
CAGTTTAATA CTGTCTTGGA ATTCATGAGA TGGAAGCATA GGTCAAAGCT GTTTGGAGAA	120
AATCAGAAGT ACAGTTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG	180
TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA	240
TTTAAATTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG GAAACATTAC	300
AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC	348
Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala	
1 5 10	
TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG	396
Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met	
15 20 25	
CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA	444
Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu	
30 35 40 45	
AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC	492
Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys	
50 55 60	
TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA	540
Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile	
65 70 75	
ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA	588
Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu	
80 85 90	
ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG	636
Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln	
95 100 105	
TGC AAA GAT TCT CCA AAA GCC CAG CTA CGC CGG ACA ATA GAA TGT TGT	684
Cys Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys	
110 115 120 125	
CGG ACC AAT TTA TGT AAC CAG TAT TTG CAA CCC ACA CTG CCC CCT GTT	732
Arg Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val	
130 135 140	
GTC ATA GGT CCG TTT TTT GAT GGC AGC ATT CGA TGG CTG GTT TTG CTC	780

Val	Ile	Gly	Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Leu	Leu	
			145					150					155			
ATT	TCT	ATG	GCT	GTC	TGC	ATA	ATT	GCT	ATG	ATC	ATC	TTC	TCC	AGC	TGC	828
Ile	Ser	Met	Ala	Val	Cys	Ile	Ile	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	
		160					165					170				
TTT	TGT	TAC	AAA	CAT	TAT	TGC	AAG	AGC	ATC	TCA	AGC	AGA	CGT	CGT	TAC	876
Phe	Cys	Tyr	Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Arg	Arg	Tyr	
	175					180					185					
AAT	CGT	GAT	TTG	GAA	CAG	GAT	GAA	GCA	TTT	ATT	CCA	GTT	GGA	GAA	TCA	924
Asn	Arg	Asp	Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	
190					195					200					205	
CTA	AAA	GAC	CTT	ATT	GAC	CAG	TCA	CAA	AGT	TCT	GGT	AGT	GGG	TCT	GGA	972
Leu	Lys	Asp	Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	
				210					215					220		
CTA	CCT	TTA	TTG	GTT	CAG	CGA	ACT	ATT	GCC	AAA	CAG	ATT	CAG	ATG	GTC	1020
Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	
			225					230					235			
CGG	CAA	GTT	GGT	AAA	GGC	CGA	TAT	GGA	GAA	GTA	TGG	ATG	GGC	AAA	TGG	1068
Arg	Gln	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	
		240					245					250				
CGT	GGC	GAA	AAA	GTG	GCG	GTG	AAA	GTA	TTC	TTT	ACC	ACT	GAA	GAA	GCC	1116
Arg	Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	
	255					260					265					
AGC	TGG	TTT	CGA	GAA	ACA	GAA	ATC	TAC	CAA	ACT	GTG	CTA	ATG	CGC	CAT	1164
Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	
270					275					280					285	
GAA	AAC	ATA	CTT	GGT	TTC	ATA	GCG	GCA	GAC	ATT	AAA	GGT	ACA	GGT	TCC	1212
Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	
				290					295					300		
TGG	ACT	CAG	CTC	TAT	TTG	ATT	ACT	GAT	TAC	CAT	GAA	AAT	GGA	TCT	CTC	1260
Trp	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	
			305					310					315			
TAT	GAC	TTC	CTG	AAA	TGT	GCT	ACA	CTG	GAC	ACC	AGA	GCC	CTG	CTT	AAA	1308
Tyr	Asp	Phe	Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	
		320					325					330				
TTG	GCT	TAT	TCA	GCT	GCC	TGT	GGT	CTG	TGC	CAC	CTG	CAC	ACA	GAA	ATT	1356
Leu	Ala	Tyr	Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	
	335					340					345					
TAT	GGC	ACC	CAA	GGA	AAG	CCC	GCA	ATT	GCT	CAT	CGA	GAC	CTA	AAG	AGC	1404
Tyr	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	
350					355					360					365	
AAA	AAC	ATC	CTC	ATC	AAG	AAA	AAT	GGG	AGT	TGC	TGC	ATT	GCT	GAC	CTG	1452
Lys	Asn	Ile	Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	
				370					375					380		
GGC	CTT	GCT	GTT	AAA	TTC	AAC	AGT	GAC	ACA	AAT	GAA	GTT	GAT	GTG	CCC	1500

Gly	Leu	Ala	Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Val	Pro	
			385					390					395			
TTG	AAT	ACC	AGG	GTG	GGC	ACC	AAA	CGC	TAC	ATG	GCT	CCC	GAA	GTG	CTG	1548
Leu	Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	
		400					405					410				
GAC	GAA	AGC	CTG	AAC	AAA	AAC	CAC	TTC	CAG	CCC	TAC	ATC	ATG	GCT	GAC	1596
Asp	Glu	Ser	Leu	Asn	Lys	Asn	His	Phe	Gln	Pro	Tyr	Ile	Met	Ala	Asp	
	415					420					425					
ATC	TAC	AGC	TTC	GGC	CTA	ATC	ATT	TGG	GAG	ATG	GCT	CGT	CGT	TGT	ATC	1644
Ile	Tyr	Ser	Phe	Gly	Leu	Ile	Ile	Trp	Glu	Met	Ala	Arg	Arg	Cys	Ile	
430					435					440					445	
ACA	GGA	GGG	ATC	GTG	GAA	GAA	TAC	CAA	TTG	CCA	TAT	TAC	AAC	ATG	GTA	1692
Thr	Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asn	Met	Val	
				450					455					460		
CCG	AGT	GAT	CCG	TCA	TAC	GAA	GAT	ATG	CGT	GAG	GTT	GTG	TGT	GTC	AAA	1740
Pro	Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met	Arg	Glu	Val	Val	Cys	Val	Lys	
			465					470					475			
CGT	TTG	CGG	CCA	ATT	GTG	TCT	AAT	CGG	TGG	AAC	AGT	GAT	GAA	TGT	CTA	1788
Arg	Leu	Arg	Pro	Ile	Val	Ser	Asn	Arg	Trp	Asn	Ser	Asp	Glu	Cys	Leu	
		480					485					490				
CGA	GCA	GTT	TTG	AAG	CTA	ATG	TCA	GAA	TGC	TGG	GCC	CAC	AAT	CCA	GCC	1836
Arg	Ala	Val	Leu	Lys	Leu	Met	Ser	Glu	Cys	Trp	Ala	His	Asn	Pro	Ala	
	495					500					505					
TCC	AGA	CTC	ACA	GCA	TTG	AGA	ATT	AAG	AAG	ACG	CTT	GCC	AAG	ATG	GTT	1884
Ser	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ala	Lys	Met	Val	
510					515					520					525	
GAA	TCC	CAA	GAT	GTA	AAA	ATC	TGATGGTTAA	ACCATCGGAG	GAGAAACTCT							1935
Glu	Ser	Gln	Asp	Val	Lys	Ile										
			530													
AGACTGCAAG	AACTGTTTTTT	ACCCATGGCA	TGGGTGGAAT	TAGAGTGGAA	TAAGGATGTT											1995
AACTTG GTTC	TCAGACTCTT	TCTTCACTAC	GTGTT CACAG	GCTGCTAATA	TTAAACCTTT											2055
CAGTACTCTT	ATTAGGATAC	AAGCTGGGAA	CTTCTAAACA	CTTCATTCTT	TATATATGGA											2115
CAGCTTTATT	TTAAATGTGG	TTTTTGATGC	CTTTTTTTTAA	GTGGGTTTTTT	ATGAACTGCA											2175
TCAAGACTTC	AATCCTGATT	AGTGTCTCCA	GTCAAGCTCT	GGGTACTGAA	TTGCCTGTTC											2235
ATAAACGGT	GCTTTCTGTG	AAAGCCTTAA	GAAGATAAAT	GAGCGCAGCA	GAGATGGAGA											2295
AATAGACTTT	GCCTTTTACC	TGAGACATTC	AGTTCGTTTG	TATTCTACCT	TTGTAAACA											2355
GCCTATAGAT	GATGATGTGT	TTGGGATACT	GCTTATTTTA	TGATAGTTTG	TCCTGTGTCC											2415
TTAGTGATGT	GTGTGTGTCT	CCATGCACAT	GCACGCCGGG	ATTCTCTGC	TGCCATTTGA											2475
ATTAGAAGAA	AATAATTTAT	ATGCATGCAC	AGGAAGATAT	TGGTGGCCGG	TGGTTTTGTG											2535
CTTTAAAAAT	GCAATATCTG	ACCAAGATTC	GCCAATCTCA													

AGTGAGATAG CTTCCCCACC AGCTTTATTT TTTAACATGA AAGCTGATGC CAAGGCCAAA 2655
AGAAGTTTAA AGCATCTGTA AATTTGGACT GTTTTCCTTC AACCACCATT TTTTTTGTGG 2715
TTATTATTTT TGTACCGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC 2775
ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCT GCATTTGATA GCAATGTAAG 2835
TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTTAAAAGGG AAGTTATTTA 2895
TATTTTGTGT ATAATGTGCT TTATTGCAA ATCACCC 2932

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Thr	Gln	Leu	Tyr	Ile	Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Tyr	Leu	Phe	1	5	10	15
Ile	Ile	Ser	Arg	Val	Gln	Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly	20	25	30	
Thr	Gly	Met	Lys	Ser	Asp	Ser	Asp	Gln	Lys	Lys	Ser	Glu	Asn	Gly	Val	35	40	45	
Thr	Leu	Ala	Pro	Glu	Asp	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser	50	55	60	
Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly	65	70	75	80
His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu	85	90	95	
Ala	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp	100	105	110	
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn	115	120	125	
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly	130	135	140	
Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Leu	Leu	Ile	Ser	Met	145	150	155	160
Ala	Val	Cys	Ile	Ile	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr	165	170	175	
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Arg	Arg	Tyr	Asn	Arg	Asp	180	185	190	
Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp	195	200	205	
Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	210	215	220	
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val	225	230	235	240
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu	245	250	255	
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	260	265	270	
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	275	280	285	
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln				

290		295		300
Leu Tyr Leu Ile Thr Asp	Tyr His Glu Asn Gly	Ser Leu Tyr Asp Phe		
305	310	315	320	
Leu Lys Cys Ala Thr	Leu Asp Thr Arg Ala	Leu Leu Lys Leu Ala Tyr		
	325	330	335	
Ser Ala Ala Cys Gly	Leu Cys His Leu His Thr	Glu Ile Tyr Gly Thr		
	340	345	350	
Gln Gly Lys Pro Ala Ile	Ala His Arg Asp Leu Lys	Ser Lys Asn Ile		
	355	360	365	
Leu Ile Lys Lys Asn Gly	Ser Cys Cys Ile Ala	Asp Leu Gly Leu Ala		
	370	375	380	
Val Lys Phe Asn Ser Asp	Thr Asn Glu Val Asp	Val Pro Leu Asn Thr		
385	390	395	400	
Arg Val Gly Thr Lys	Arg Tyr Met Ala Pro	Glu Val Leu Asp Glu Ser		
	405	410	415	
Leu Asn Lys Asn His Phe	Gln Pro Tyr Ile Met	Ala Asp Ile Tyr Ser		
	420	425	430	
Phe Gly Leu Ile Ile Trp	Glu Met Ala Arg Arg	Cys Ile Thr Gly Gly		
	435	440	445	
Ile Val Glu Glu Tyr Gln	Leu Pro Tyr Tyr Asn	Met Val Pro Ser Asp		
	450	455	460	
Pro Ser Tyr Glu Asp Met	Arg Glu Val Val Cys	Val Lys Arg Leu Arg		
465	470	475	480	
Pro Ile Val Ser Asn	Arg Trp Asn Ser Asp	Glu Cys Leu Arg Ala Val		
	485	490	495	
Leu Lys Leu Met Ser Glu	Cys Trp Ala His Asn	Pro Ala Ser Arg Leu		
	500	505	510	
Thr Ala Leu Arg Ile Lys	Lys Thr Leu Ala Lys	Met Val Glu Ser Gln		
	515	520	525	
Asp Val Lys Ile				
530				

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT GTT GTC CTC	
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu	
1 5 10 15	

CTG	CTC	GCC	GGC	AGC	GGC	GGG	TCC	GGG	CCC	CGG	GGG	GTC	CAG	GCT	CTG	96
Leu	Leu	Ala	Gly	Ser	Gly	Gly	Ser	Gly	Pro	Arg	Gly	Val	Gln	Ala	Leu	
			20					25					30			
CTG	TGT	GCG	TGC	ACC	AGC	TGC	CTC	CAG	GCC	AAC	TAC	ACG	TGT	GAG	ACA	144
Leu	Cys	Ala	Cys	Thr	Ser	Cys	Leu	Gln	Ala	Asn	Tyr	Thr	Cys	Glu	Thr	
		35					40					45				
GAT	GGG	GCC	TGC	ATG	GTT	TCC	TTT	TTC	AAT	CTG	GAT	GGG	ATG	GAG	CAC	192
Asp	Gly	Ala	Cys	Met	Val	Ser	Phe	Phe	Asn	Leu	Asp	Gly	Met	Glu	His	
	50					55					60					
CAT	GTG	CGC	ACC	TGC	ATC	CCC	AAA	GTG	GAG	CTG	GTC	CCT	GCC	GGG	AAG	240
His	Val	Arg	Thr	Cys	Ile	Pro	Lys	Val	Glu	Leu	Val	Pro	Ala	Gly	Lys	
	65				70					75					80	
CCC	TTC	TAC	TGC	CTG	AGC	TCG	GAG	GAC	CTG	CGC	AAC	ACC	CAC	TGC	TGC	288
Pro	Phe	Tyr	Cys	Leu	Ser	Ser	Glu	Asp	Leu	Arg	Asn	Thr	His	Cys	Cys	
				85				90						95		
TAC	ACT	GAC	TAC	TGC	AAC	AGG	ATC	GAC	TTG	AGG	GTG	CCC	AGT	GGT	CAC	336
Tyr	Thr	Asp	Tyr	Cys	Asn	Arg	Ile	Asp	Leu	Arg	Val	Pro	Ser	Gly	His	
			100					105					110			
CTC	AAG	GAG	CCT	GAG	CAC	CCG	TCC	ATG	TGG	GGC	CCG	GTG	GAG	CTG	GTA	384
Leu	Lys	Glu	Pro	Glu	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val	
		115					120					125				
GGC	ATC	ATC	GCC	GGC	CCG	GTG	TTC	CTC	CTG	TTC	CTC	ATC	ATC	ATC	ATT	432
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile	
	130					135					140					
GTT	TTC	CTT	GTC	ATT	AAC	TAT	CAT	CAG	CGT	GTC	TAT	CAC	AAC	CGC	CAG	480
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln	
	145				150					155					160	
AGA	CTG	GAC	ATG	GAA	GAT	CCC	TCA	TGT	GAG	ATG	TGT	CTC	TCC	AAA	GAC	528
Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp	
				165					170					175		
AAG	ACG	CTC	CAG	GAT	CTT	GTC	TAC	GAT	CTC	TCC	ACC	TCA	GGG	TCT	GGC	576
Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly	
			180					185					190			
TCA	GGG	TTA	CCC	CTC	TTT	GTC	CAG	CGC	ACA	GTG	GCC	CGA	ACC	ATC	GTT	624
Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val	
		195					200					205				
TTA	CAA	GAG	ATT	ATT	GGC	AAG	GGT	CGG	TTT	GGG	GAA	GTA	TGG	CGG	GGC	672
Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly	
	210					215					220					
CGC	TGG	AGG	GGT	GGT	GAT	GTG	GCT	GTG	AAA	ATA	TTC	TCT	TCT	CGT	GAA	720
Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu	
	225				230					235					240	
GAA	CGG	TCT	TGG	TTC	AGG	GAA	GCA	GAG	ATA	TAC	CAG	ACG	GTC	ATG	CTG	768
Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	
				245					250					255		
CGC	CAT	GAA	AAC	ATC	CTT	GGA	TTT	ATT	GCT	GCT	GAC	AAT	AAA	GAT	AAT	816

Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn	
			260					265					270			
GGC	ACC	TGG	ACA	CAG	CTG	TGG	CTT	GTT	TCT	GAC	TAT	CAT	GAG	CAC	GGG	864
Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly	
		275					280					285				
TCC	CTG	TTT	GAT	TAT	CTG	AAC	CGG	TAC	ACA	GTG	ACA	ATT	GAG	GGG	ATG	912
Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	Glu	Gly	Met	
	290					295					300					
ATT	AAG	CTG	GCC	TTG	TCT	GCT	GCT	AGT	GGG	CTG	GCA	CAC	CTG	CAC	ATG	960
Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met	
305					310				315						320	
GAG	ATC	GTG	GGC	ACC	CAA	GGG	AAG	CCT	GGA	ATT	GCT	CAT	CGA	GAC	TTA	1008
Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	Arg	Asp	Leu	
			325						330					335		
AAG	TCA	AAG	AAC	ATT	CTG	GTG	AAG	AAA	AAT	GGC	ATG	TGT	GCC	ATA	GCA	1056
Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	Ala	Ile	Ala	
			340					345					350			
GAC	CTG	GGC	CTG	GCT	GTC	CGT	CAT	GAT	GCA	GTC	ACT	GAC	ACC	ATT	GAC	1104
Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	Thr	Ile	Asp	
		355					360					365				
ATT	GCC	CCG	AAT	CAG	AGG	GTG	GGG	ACC	AAA	CGA	TAC	ATG	GCC	CCT	GAA	1152
Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	
	370					375					380					
GTA	CTT	GAT	GAA	ACC	ATT	AAT	ATG	AAA	CAC	TTT	GAC	TCC	TTT	AAA	TGT	1200
Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	Phe	Lys	Cys	
385					390					395					400	
GCT	GAT	ATT	TAT	GCC	CTC	GGG	CTT	GTA	TAT	TGG	GAG	ATT	GCT	CGA	AGA	1248
Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	Glu	Ile	Ala	Arg	Arg	
				405				410						415		
TGC	AAT	TCT	GGA	GGA	GTC	CAT	GAA	GAA	TAT	CAG	CTG	CCA	TAT	TAC	GAC	1296
Cys	Asn	Ser	Gly	Gly	Val	His	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asp	
			420					425					430			
TTA	GTG	CCC	TCT	GAC	CCT	TCC	ATT	GAG	GAA	ATG	CGA	AAG	GTT	GTA	TGT	1344
Leu	Val	Pro	Ser	Asp	Pro	Ser	Ile	Glu	Glu	Met	Arg	Lys	Val	Val	Cys	
		435					440					445				
GAT	CAG	AAG	CTG	CGT	CCC	AAC	ATC	CCC	AAC	TGG	TGG	CAG	AGT	TAT	GAG	1392
Asp	Gln	Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Trp	Trp	Gln	Ser	Tyr	Glu	
	450					455					460					
GCA	CTG	CGG	GTG	ATG	GGG	AAG	ATG	ATG	CGA	GAG	TGT	TGG	TAT	GCC	AAC	1440
Ala	Leu	Arg	Val	Met	Gly	Lys	Met	Met	Arg	Glu	Cys	Trp	Tyr	Ala	Asn	
465					470					475					480	

GGC GCA GCC CGC CTG ACG GCC CTG CGC ATC AAG AAG ACC CTC TCC CAG	1488
Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln	
485 490 495	
CTC AGC GTG CAG GAA GAC GTG AAG ATC TAACTGCTCC CTCTCTCCAC	1535
Leu Ser Val Gln Glu Asp Val Lys Ile	
500 505	
ACGGAGCTCC TGGCAGCGAG AACTACGCAC AGCTGCCGCG TTGAGCGTAC GATGGAGGCC	1595
TACCTCTCGT TTCTGCCCAG CCCTCTGTGG CCAGGAGCCC TGGCCCGCAA GAGGGACAGA	1655
GCCCGGGAGA GACTCGCTCA CTCCCATGTT GGGTTTGAGA CAGACACCTT TTCTATTTAC	1715
CTCCTAATGG CATGGAGACT CTGAGAGCGA ATTGTGTGGA GAACTCAGTG CCACACCTCG	1775
AACTGGTTGT AGTGGGAAGT CCCGCGAAAC CCGGTGCATC TGGCACGTGG CCAGGAGCCA	1835
TGACAGGGGC GCTTGGGAGG GGCCGGAGGA ACCGAGGTGT TGCCAGTGCT AAGCTGCCCT	1895
GAGGGTTTCC TTCGGGGACC AGCCCACAGC ACACCAAGGT GGCCCGGAAG AACCAGAAGT	1955
GCAGCCCCTC TCACAGGCAG CTCTGAGCCG CGCTTTCCCC TCCTCCCTGG GATGGACGCT	2015
GCCGGGAGAC TGCCAGTGGA GACGGAATCT GCCGCTTGT CTGTCCAGCC GTGTGTGCAT	2075
GTGCCGAGGT GCGTCCCCCG TTGTGCCTGG TTCGTGCCAT GCCCTTACAC GTGCGTGTGA	2135
GTGTGTGTGT GTGTCTGTAG GTGCGCACTT ACCTGCTTGA GCTTTCTGTG CATGTGCAGG	2195
TCGGGGGTGT GGTCGTCATG CTGTCCGTGC TTGCTGGTGC CTCTTTTCAG TAGTGAGCAG	2255
CATCTAGTTT CCCTGGTGCC CTTCCCTGGA GGTCTCTCCC TCCCCCAGAG CCCCTCATGC	2315
CACAGTGGTA CTCTGTGT	2333

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 505 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Ala	Glu	Ser	Ala	Gly	Ala	Ser	Ser	Phe	Phe	Pro	Leu	Val	Val	Leu
1				5					10					15	
Leu	Leu	Ala	Gly	Ser	Gly	Gly	Ser	Gly	Pro	Arg	Gly	Val	Gln	Ala	Leu
		20						25					30		
Leu	Cys	Ala	Cys	Thr	Ser	Cys	Leu	Gln	Ala	Asn	Tyr	Thr	Cys	Glu	Thr
		35					40					45			
Asp	Gly	Ala	Cys	Met	Val	Ser	Phe	Phe	Asn	Leu	Asp	Gly	Met	Glu	His
	50					55				60					
His	Val	Arg	Thr	Cys	Ile	Pro	Lys	Val	Glu	Leu	Val	Pro	Ala	Gly	Lys
	65				70					75				80	
Pro	Phe	Tyr	Cys	Leu	Ser	Ser	Glu	Asp	Leu	Arg	Asn	Thr	His	Cys	Cys
			85						90					95	

Tyr	Thr	Asp	Tyr	Cys	Asn	Arg	Ile	Asp	Leu	Arg	Val	Pro	Ser	Gly	His
			100					105					110		
Leu	Lys	Glu	Pro	Glu	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val
		115					120					125			
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile
		130				135					140				
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln
145					150					155					160
Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp
			165						170					175	
Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly
		180						185					190		
Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val
		195					200				205				
Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly
		210				215					220				
Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu
225					230					235					240
Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu
				245					250					255	
Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn
			260					265					270		
Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly
		275					280					285			
Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	Glu	Gly	Met
		290				295					300				
Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met
305					310					315					320
Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	Arg	Asp	Leu
				325					330					335	
Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	Ala	Ile	Ala
			340					345					350		
Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	Thr	Ile	Asp
		355					360					365			
Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu
		370				375					380				
Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	Phe	Lys	Cys
385					390					395					400
Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	Glu	Ile	Ala	Arg	Arg
				405					410					415	
Cys	Asn	Ser	Gly	Gly	Val	His	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asp
			420					425					430		
Leu	Val	Pro	Ser	Asp	Pro	Ser	Ile	Pro	Asn	Trp	Trp	Gln	Ser	Tyr	Glu
		435					440						445		
Asp	Gln	Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Trp	Trp	Gln	Ser	Tyr	Glu
		450				455					460				
Ala	Leu	Arg	Val	Met	Gly	Lys	Met	Met	Arg	Glu	Cys	Trp	Tyr	Ala	Asn
465					470					475					480
Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ser	Gln
				485					490					495	
Leu	Ser	Val	Gln	Glu	Asp	Val	Lys	Ile							
			500					505							

- (2) INFORMATION FOR SEQ ID NO: 9:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mouse

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 77..1585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCGAGGCGA GGTTCGCTGG GGTGAGGCAG CGGCGCGGCC GGGCCGGGCC GGGCCACAGG	60
CGGTGGCGGC GGGACC ATG GAG GCG GCG GTC GCT GCT CCG CGT CCC CGG	109
Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg	
1 5 10	
CTG CTC CTC CTC GTG CTG GCG GCG GCG GCG GCG GCG GCG GCG GCG CTG	157
Leu Leu Leu Leu Val Leu Ala Ala Ala Ala Ala Ala Ala Ala Leu	
15 20 25	
CTC CCG GGG GCG ACG GCG TTA CAG TGT TTC TGC CAC CTC TGT ACA AAA	205
Leu Pro Gly Ala Thr Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys	
30 35 40	
GAC AAT TTT ACT TGT GTG ACA GAT GGG CTC TGC TTT GTC TCT GTC ACA	253
Asp Asn Phe Thr Cys Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr	
45 50 55	
GAG ACC ACA GAC AAA GTT ATA CAC AAC AGC ATG TGT ATA GCT GAA ATT	301
Glu Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile	
60 65 70 75	
GAC TTA ATT CCT CGA GAT AGG CCG TTT GTA TGT GCA CCC TCT TCA AAA	349
Asp Leu Ile Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys	
80 85 90	
ACT GGG TCT GTG ACT ACA ACA TAT TGC TGC AAT CAG GAC CAT TGC AAT	397
Thr Gly Ser Val Thr Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn	
95 100 105	
AAA ATA GAA CTT CCA ACT ACT GTA AAG TCA TCA CCT GGC CTT GGT CCT	445
Lys Ile Glu Leu Pro Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro	
110 115 120	
GTG GAA CTG GCA GCT GTC ATT GCT GGA CCA GTG TGC TTC GTC TGC ATC	493
Val Glu Leu Ala Ala Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile	
125 130 135	
TCA CTC ATG TTG ATG GTC TAT ATC TGC CAC AAC CGC ACT GTC ATT CAC	541
Ser Leu Met Leu Met Val Tyr Ile Cys His Asn Arg Thr Val Ile His	
140 145 150 155	
CAT CGA GTG CCA AAT GAA GAG GAC CCT TCA TTA GAT CGC CCT TTT ATT	589

His	Arg	Val	Pro	Asn	Glu	Glu	Asp	Pro	Ser	Leu	Asp	Arg	Pro	Phe	Ile	
				160					165					170		
TCA	GAG	GGT	ACT	ACG	TTG	AAA	GAC	TTA	ATT	TAT	GAT	ATG	ACA	ACG	TCA	637
Ser	Glu	Gly	Thr	Thr	Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Met	Thr	Thr	Ser	
			175					180					185			
GGT	TCT	GGC	TCA	GGT	TTA	CCA	TTG	CTT	GTT	CAG	AGA	ACA	ATT	GCG	AGA	685
Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Arg	
		190					195					200				
ACT	ATT	GTG	TTA	CAA	GAA	AGC	ATT	GGC	AAA	GGT	CGA	TTT	GGA	GAA	GTT	733
Thr	Ile	Val	Leu	Gln	Glu	Ser	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	
	205					210					215					
TGG	AGA	GGA	AAG	TGG	CGG	GGA	GAA	GAA	GTT	GCT	GTT	AAG	ATA	TTC	TCC	781
Trp	Arg	Gly	Lys	Trp	Arg	Gly	Glu	Glu	Val	Ala	Val	Lys	Ile	Phe	Ser	
220					225					230					235	
TCT	AGA	GAA	GAA	CGT	TCG	TGG	TTC	CGT	GAG	GCA	GAG	ATT	TAT	CAA	ACT	829
Ser	Arg	Glu	Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	
				240					245					250		
GTA	ATG	TTA	CGT	CAT	GAA	AAC	ATC	CTG	GGA	TTT	ATA	GCA	GCA	GAC	AAT	877
Val	Met	Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	
			255					260						265		
AAA	GAC	AAT	GGT	ACT	TGG	ACT	CAG	CTC	TGG	TTG	GTG	TCA	GAT	TAT	CAT	925
Lys	Asp	Asn	Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	
		270					275					280				
GAG	CAT	GGA	TCC	CTT	TTT	GAT	TAC	TTA	AAC	AGA	TAC	ACA	GTT	ACT	GTG	973
Glu	His	Gly	Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Val	
	285					290					295					
GAA	GGA	ATG	ATA	AAA	CTT	GCT	CTG	TCC	ACG	GCG	AGC	GGT	CTT	GCC	CAT	1021
Glu	Gly	Met	Ile	Lys	Leu	Ala	Leu	Ser	Thr	Ala	Ser	Gly	Leu	Ala	His	
300					305					310					315	
CTT	CAC	ATG	GAG	ATT	GTT	GGT	ACC	CAA	GGA	AAG	CCA	GCC	ATT	GCT	CAT	1069
Leu	His	Met	Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	
			320						325					330		
AGA	GAT	TTG	AAA	TCA	AAG	AAT	ATC	TTG	GTA	AAG	AAG	AAT	GGA	ACT	TGC	1117
Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	
			335					340					345			
TGT	ATT	GCA	GAC	TTA	GGA	CTG	GCA	GTA	AGA	CAT	GAT	TCA	GCC	ACA	GAT	1165
Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ser	Ala	Thr	Asp	
		350					355					360				
ACC	ATT	GAT	ATT	GCT	CCA	AAC	CAC	AGA	GTG	GGA	ACA	AAA	AGG	TAC	ATG	1213
Thr	Ile	Asp	Ile	Ala	Pro	Asn	His	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	
	365					370					375					
GCC	CCT	GAA	GTT	CTC	GAT	GAT	TCC	ATA	AAT	ATG	AAA	CAT	TTT	GAA	TCC	1261
Ala	Pro	Glu	Val	Leu	Asp	Asp	Ser	Ile	Asn	Met	Lys	His	Phe	Glu	Ser	
380					385					390					395	
TTC	AAA	CGT	GCT	GAC	ATC	TAT	GCA	ATG	GGC	TTA	GTA	TTC	TGG	GAA	ATT	1309

Phe	Lys	Arg	Ala	Asp	Ile	Tyr	Ala	Met	Gly	Leu	Val	Phe	Trp	Glu	Ile		
				400					405					410			
GCT	CGA	CGA	TGT	TCC	ATT	GGT	GGA	ATT	CAT	GAA	GAT	TAC	CAA	CTG	CCT	1357	
Ala	Arg	Arg	Cys	Ser	Ile	Gly	Gly	Ile	His	Glu	Asp	Tyr	Gln	Leu	Pro		
			415					420					425				
TAT	TAT	GAT	CTT	GTA	CCT	TCT	GAC	CCA	TCA	GTT	GAA	GAA	ATG	AGA	AAA	1405	
Tyr	Tyr	Asp	Leu	Val	Pro	Ser	Asp	Pro	Ser	Val	Glu	Glu	Met	Arg	Lys		
		430					435					440					
GTT	GTT	TGT	GAA	CAG	AAG	TTA	AGG	CCA	AAT	ATC	CCA	AAC	AGA	TGG	CAG	1453	
Val	Val	Cys	Glu	Gln	Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Arg	Trp	Gln		
		445					450					455					
AGC	TGT	GAA	GCC	TTG	AGA	GTA	ATG	GCT	AAA	ATT	ATG	AGA	GAA	TGT	TGG	1501	
Ser	Cys	Glu	Ala	Leu	Arg	Val	Met	Ala	Lys	Ile	Met	Arg	Glu	Cys	Trp		
460					465					470					475		
TAT	GCC	AAT	GGA	GCA	GCT	AGG	CTT	ACA	GCA	TTG	CGG	ATT	AAG	AAA	ACA	1549	
Tyr	Ala	Asn	Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr		
				480					485					490			
TTA	TCG	CAA	CTC	AGT	CAA	CAG	GAA	GGC	ATC	AAA	ATG	TAATTCTACA				1595	
Leu	Ser	Gln	Leu	Ser	Gln	Gln	Glu	Gly	Ile	Lys	Met						
			495					500									
GCTTTGCCTG	AACTCTCCTT	TTTTCTTCAG	ATCTGCTCCT	GGGTTTTAAT	TTGGGAGGTC											1655	
AGTTGTTCTA	CCTCACTGAG	AGGGAACAGA	AGGATATTGC	TTCCTTTTGC	AGCAGTGTA											1715	
TAAAGTCAAT	TAAAAACTTC	CCAGGATTTC	TTTGGACCCA	GGAAACAGCC	ATGTGGGTCC											1775	
TTTCTGTGCA	CTATGAACGC	TTCTTTCCCA	GGACAGAAAA	TGTGTAGTCT	ACCTTTATTT											1835	
TTTATTAACA	AAACTTGTTT	TTTAAAAAGA	TGATTGCTGG	TCTTAACTTT	AGGTAACCTCT											1895	
GCTGTGCTGG	AGATCATCTT	TAAGGGCAAA	GGAGTTGGAT	TGCTGAATTA	CAATGAAACA											1955	
TGTCTTATTA	CTAAAGAAAG	TGATTTACTC	CTGGTTAGTA	CATTCTCAGA	GGATTCTGAA											2015	
CCACTAGAGT	TTCCTTGATT	CAGACTTTGA	ATGTACTGTT	CTATAGTTTT	TCAGGATCTT											2075	
AAAATAACA	CTTATAAAAC	TCTTATCTTG	AGTCTAAAAA	TGACCTCATA	TAGTAGTGAG											2135	
GAACATAATT	CATGCAATTG	TATTTTGTAT	ACTATTATTG	TTCTTTCACT	TATTCAGAAC											2195	
ATTACATGCC	TTCAAAATGG	GATTGTACTA	TACCAGTAAG	TGCCACTTCT	GTGTCTTTCT											2255	
AATGGAAATG	AGTAGAATTG	CTGAAAGTCT	CTATGTTAAA	ACCTATAGTG	TTT											2308	

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Glu	Ala	Ala	Val	Ala	Ala	Pro	Arg	Pro	Arg	Leu	Leu	Leu	Leu	Val
1				5					10					15	
Leu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Pro	Gly	Ala	Thr
			20					25					30		
Ala	Leu	Gln	Cys	Phe	Cys	His	Leu	Cys	Thr	Lys	Asp	Asn	Phe	Thr	Cys
		35					40					45			
Val	Thr	Asp	Gly	Leu	Cys	Phe	Val	Ser	Val	Thr	Glu	Thr	Thr	Asp	Lys
	50					55					60				
Val	Ile	His	Asn	Ser	Met	Cys	Ile	Ala	Glu	Ile	Asp	Leu	Ile	Pro	Arg
65					70					75				80	
Asp	Arg	Pro	Phe	Val	Cys	Ala	Pro	Ser	Ser	Lys	Thr	Gly	Ser	Val	Thr
			85						90					95	
Thr	Thr	Tyr	Cys	Cys	Asn	Gln	Asp	His	Cys	Asn	Lys	Ile	Glu	Leu	Pro
			100					105					110		
Thr	Thr	Val	Lys	Ser	Ser	Pro	Gly	Leu	Gly	Pro	Val	Glu	Leu	Ala	Ala
		115					120					125			
Val	Ile	Ala	Gly	Pro	Val	Cys	Phe	Val	Cys	Ile	Ser	Leu	Met	Leu	Met
130						135					140				
Val	Tyr	Ile	Cys	His	Asn	Arg	Thr	Val	Ile	His	His	Arg	Val	Pro	Asn
145					150					155				160	
Glu	Glu	Asp	Pro	Ser	Leu	Asp	Arg	Pro	Phe	Ile	Ser	Glu	Gly	Thr	Thr
			165						170					175	
Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Met	Thr	Thr	Ser	Gly	Ser	Gly	Ser	Gly
		180					185						190		
Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Arg	Thr	Ile	Val	Leu	Gln
	195						200					205			
Glu	Ser	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly	Lys	Trp
210					215						220				
Arg	Gly	Glu	Glu	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu	Glu	Arg
225					230					235				240	
Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	Arg	His
			245						250				255		
Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn	Gly	Thr
		260					265						270		
Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly	Ser	Leu
	275						280					285			
Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Val	Glu	Gly	Met	Ile	Lys
290					295						300				
Leu	Ala	Leu	Ser	Thr	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met	Glu	Ile
305					310					315				320	
Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser
			325						330				335		
Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu
		340					345						350		
Gly	Leu	Ala	Val	Arg	His	Asp	Ser	Ala	Thr	Asp	Thr	Ile	Asp	Ile	Ala
	355						360					365			
Pro	Asn	His	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu
370					375						380				
Asp	Asp	Ser	Ile	Asn	Met	Lys	His	Phe	Glu	Ser	Phe	Lys	Arg	Ala	Asp
385				390						395				400	
Ile	Tyr	Ala	Met	Gly	Leu	Val	Phe	Trp	Glu	Ile	Ala	Arg	Arg	Cys	Ser
			405						410					415	
Ile	Gly	Gly	Ile	His	Glu	Asp	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asp	Leu	Val
		420					425						430		
Pro	Ser	Asp	Pro	Ser	Val	Glu	Glu	Met	Arg	Lys	Val	Val	Cys	Glu	Gln
	435						440						445		
Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Arg	Trp	Gln	Ser	Cys	Glu	Ala	Leu
	450					455						460			

Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala
 465 470 475 480
 Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser
 485 490 495
 Gln Gln Glu Gly Ile Lys Met
 500

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 241..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAGAGCACAG CCCTTCCCAG TCCCCGAGC CGCCGCGCCA CGCGCGCATG ATCAAGACCT	60
TTTCCCCGGC CCCACAGGGC CTCTGGACGT GAGACCCCGG CCGCCTCCGC AAGGAGAGGC	120
GGGGGTGCGAG TCGCCCTGTC CAAAGGCCTC AATCTAAACA ATCTTGATTC CTGTTGCCGG	180
CTGGCGGGAC CCTGAATGGC AGGAAATCTC ACCACATCTC TTCTCCTATC TCCAAGGACC	240
ATG ACC TTG GGG AGC TTC AGA AGG GGC CTT TTG ATG CTG TCG GTG GCC	288
Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala	
1 5 10 15	
TTG GGC CTA ACC CAG GGG AGA CTT GCG AAG CCT TCC AAG CTG GTG AAC	336
Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn	
20 25 30	
TGC ACT TGT GAG AGC CCA CAC TGC AAG AGA CCA TTC TGC CAG GGG TCA	384
Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser	
35 40 45	
TGG TGC ACA GTG GTG CTG GTT CGA GAG CAG GGC AGG CAC CCC CAG GTC	432
Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val	
50 55 60	
TAT CGG GGC TGT GGG AGC CTG AAC CAG GAG CTC TGC TTG GGA CGT CCC	480
Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro	
65 70 75 80	

ACG GAG TTT CTG AAC CAT CAC TGC TGC TAT AGA TCC TTC TGC AAC CAC	528
Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His	
85 90 95	
AAC GTG TCT CTG ATG CTG GAG GCC ACC CAA ACT CCT TCG GAG GAG CCA	576
Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro	
100 105 110	
GAA GTT GAT GCC CAT CTG CCT CTG ATC CTG GGT CCT GTG CTG GCC TTG	624
Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu	
115 120 125	
CCG GTC CTG GTG GCC CTG GGT GCT CTG GGC TTG TGG CGT GTC CGG CGG	672
Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg	
130 135 140	
AGG CAG GAG AAG CAG CGG GAT TTG CAC AGT GAC CTG GGC GAG TCC AGT	720
Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser	
145 150 155 160	
CTC ATC CTG AAG GCA TCT GAA CAG GCA GAC AGC ATG TTG GGG GAC TTC	768
Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe	
165 170 175	
CTG GAC AGC GAC TGT ACC ACG GGC AGC GGC TCG GGG CTC CCC TTC TTG	816
Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu	
180 185 190	
GTG CAG AGG ACG GTA GCT CGG CAG GTT GCG CTG GTA GAG TGT GTG GGA	864
Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly	
195 200 205	
AAG GGC CGA TAT GGC GAG GTG TGG CGC GGT TCG TGG CAT GGC GAA AGC	912
Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser	
210 215 220	
GTG GCG GTC AAG ATT TTC TCC TCA CGA GAT GAG CAG TCC TGG TTC CGG	960
Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg	
225 230 235 240	
GAG ACG GAG ATC TAC AAC ACA GTT CTG CTT AGA CAC GAC AAC ATC CTA	1008
Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu	
245 250 255	
GGC TTC ATC GCC TCC GAC ATG ACT TCG CGG AAC TCG AGC ACG CAG CTG	1056
Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu	
260 265 270	
TGG CTC ATC ACC CAC TAC CAT GAA CAC GGC TCC CTC TAT GAC TTT CTG	1104
Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu	
275 280 285	
CAG AGG CAG ACG CTG GAG CCC CAG TTG GCC CTG AGG CTA GCT GTG TCC	1152
Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser	
290 295 300	
CCG GCC TGC GGC CTG GCG CAC CTA CAT GTG GAG ATC TTT GGC ACT CAA	1200
Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln	
305 310 315 320	

GGC AAA CCA GCC ATT GCC CAT CGT GAC CTC AAG AGT CGC AAT GTG CTG Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu 325 330 335	1248
GTC AAG AGT AAC TTG CAG TGT TGC ATT GCA GAC CTG GGA CTG GCT GTG Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val 340 345 350	1296
ATG CAC TCA CAA AGC AAC GAG TAC CTG GAT ATC GGC AAC ACA CCC CGA Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg 355 360 365	1344
GTG GGT ACC AAA AGA TAC ATG GCA CCC GAG GTG CTG GAT GAG CAC ATC Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile 370 375 380	1392
CGC ACA GAC TGC TTT GAG TCG TAC AAG TGG ACA GAC ATC TGG GCC TTT Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe 385 390 395 400	1440
GGC CTA GTG CTA TGG GAG ATC GCC CGG CGG ACC ATC ATC AAT GGC ATT Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile 405 410 415	1488
GTG GAG GAT TAC AGG CCA CCT TTC TAT GAC ATG GTA CCC AAT GAC CCC Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro 420 425 430	1536
AGT TTT GAG GAC ATG AAA AAG GTG GTG TGC GTT GAC CAG CAG ACA CCC Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro 435 440 445	1584
ACC ATC CCT AAC CGG CTG GCT GCA GAT CCG GTC CTC TCC GGG CTG GCC Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala 450 455 460	1632
CAG ATG ATG AGA GAG TGC TGG TAC CCC AAC CCC TCT GCT CGC CTC ACC Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr 465 470 475 480	1680
GCA CTG CGC ATA AAG AAG ACA TTG CAG AAG CTC AGT CAC AAT CCA GAG Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu 485 490 495	1728
AAG CCC AAA GTG ATT CAC TAGCCCAGGG CCACCAGGCT TCCTCTGCCT Lys Pro Lys Val Ile His 500	1776
AAAGTGTGTG CTGGGGAAGA AGACATAGCC TGTCTGGGTA GAGGGAGTGA AGAGAGTGTG	1836
CACGCTGCCC TGTGTGTGCC TGCTCAGCTT GCTCCCAGCC CATCCAGCCA AAAATACAGC	1896
TGAGCTGAAA TTCAAAAAAA AAAAAA	1922

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Thr	Leu	Gly	Ser	Phe	Arg	Arg	Gly	Leu	Leu	Met	Leu	Ser	Val	Ala	
1				5				10						15		
Leu	Gly	Leu	Thr	Gln	Gly	Arg	Leu	Ala	Lys	Pro	Ser	Lys	Leu	Val	Asn	
			20					25					30			
Cys	Thr	Cys	Glu	Ser	Pro	His	Cys	Lys	Arg	Pro	Phe	Cys	Gln	Gly	Ser	
		35					40					45				
Trp	Cys	Thr	Val	Val	Leu	Val	Arg	Glu	Gln	Gly	Arg	His	Pro	Gln	Val	
	50					55					60					
Tyr	Arg	Gly	Cys	Gly	Ser	Leu	Asn	Gln	Glu	Leu	Cys	Leu	Gly	Arg	Pro	
65					70					75					80	
Thr	Glu	Phe	Leu	Asn	His	His	Cys	Cys	Tyr	Arg	Ser	Phe	Cys	Asn	His	
				85					90					95		
Asn	Val	Ser	Leu	Met	Leu	Glu	Ala	Thr	Gln	Thr	Pro	Ser	Glu	Glu	Pro	
			100					105					110			
Glu	Val	Asp	Ala	His	Leu	Pro	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu	
		115					120					125				
Pro	Val	Leu	Val	Ala	Leu	Gly	Ala	Leu	Gly	Leu	Trp	Arg	Val	Arg	Arg	
	130					135					140					
Arg	Gln	Glu	Lys	Gln	Arg	Asp	Leu	His	Ser	Asp	Leu	Gly	Glu	Ser	Ser	
145					150					155					160	
Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Ala	Asp	Ser	Met	Leu	Gly	Asp	Phe	
				165					170					175		
Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	
			180					185					190			
Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	
		195					200					205				
Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Ser	Trp	His	Gly	Glu	Ser	
	210					215					220					
Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg	
225					230					235					240	
Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu	
				245					250					255		
Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu	
			260					265						270		
Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	
		275					280						285			
Gln	Arg	Gln	Thr	Leu	Glu	Pro	Gln	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser	
	290					295					300					
Pro	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln	
305					310					315					320	
Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Arg	Asn	Val	Leu	
				325					330					335		
Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	
			340					345					350			
Met	His	Ser	Gln	Ser	Asn	Glu	Tyr	Leu	Asp	Ile	Gly	Asn	Thr	Pro	Arg	
		355					360						365			
Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	His	Ile	
	370					375					380					
Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala	Phe	
385					390					395					400	
Gly	Leu	Val	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Thr	Ile	Ile	Asn	Gly	Ile	
				405					410					415		
Val	Glu	Asp	Tyr	Arg	Pro	Pro	Phe	Tyr	Asp	Met	Val	Pro	Asn	Asp	Pro	
			420					425					430			
Ser	Phe	Glu	Asp	Met	Lys	Lys	Val	Val	Cys	Val	Asp	Gln	Gln	Thr	Pro	
		435					440						445			

Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly	His	Cys	Phe	Ala	Ile	Ile		
				75					80					85			
GAA	GAA	GAT	GAT	CAG	GGA	GAA	ACC	ACA	TTA	ACT	TCT	GGG	TGT	ATG	AAG	522	
Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu	Thr	Ser	Gly	Cys	Met	Lys		
			90					95					100				
TAT	GAA	GGC	TCT	GAT	TTT	CAA	TGC	AAG	GAT	TCA	CCG	AAA	GCC	CAG	CTA	570	
Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp	Ser	Pro	Lys	Ala	Gln	Leu		
		105					110					115					
CGC	AGG	ACA	ATA	GAA	TGT	TGT	CGG	ACC	AAT	TTG	TGC	AAC	CAG	TAT	TTG	618	
Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn	Leu	Cys	Asn	Gln	Tyr	Leu		
		120				125					130						
CAG	CCT	ACA	CTG	CCC	CCT	GTT	GTT	ATA	GGT	CCG	TTC	TTT	GAT	GGC	AGC	666	
Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly	Pro	Phe	Phe	Asp	Gly	Ser		
					140				145						150		
ATC	CGA	TGG	CTG	GTT	GTG	CTC	ATT	TCC	ATG	GCT	GTC	TGT	ATA	GTT	GCT	714	
Ile	Arg	Trp	Leu	Val	Val	Leu	Ile	Ser	Met	Ala	Val	Cys	Ile	Val	Ala		
				155					160					165			
ATG	ATC	ATC	TTC	TCC	AGC	TGC	TTT	TGC	TAT	AAG	CAT	TAT	TGT	AAG	AGT	762	
Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr	Lys	His	Tyr	Cys	Lys	Ser		
			170					175					180				
ATC	TCA	AGC	AGG	GGT	CGT	TAC	AAC	CGT	GAT	TTG	GAA	CAG	GAT	GAA	GCA	810	
Ile	Ser	Ser	Arg	Gly	Arg	Tyr	Asn	Arg	Asp	Leu	Glu	Gln	Asp	Glu	Ala		
			185				190					195					
TTT	ATT	CCA	GTA	GGA	GAA	TCA	TTG	AAA	GAC	CTG	ATT	GAC	CAG	TCC	CAA	858	
Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp	Leu	Ile	Asp	Gln	Ser	Gln		
	200					205					210						
AGC	TCT	GGG	AGT	GGA	TCT	GGA	TTG	CCT	TTA	TTG	GTT	CAG	CGA	ACT	ATT	906	
Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile		
					220					225					230		
GCC	AAA	CAG	ATT	CAG	ATG	GTT	CGG	CAG	GTT	GGT	AAA	GGC	CGC	TAT	GGA	954	
Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val	Gly	Lys	Gly	Arg	Tyr	Gly		
				235				240						245			
GAA	GTA	TGG	ATG	GGT	AAA	TGG	CGT	GGT	GAA	AAA	GTG	GCT	GTC	AAA	GTG	1002	
Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu	Lys	Val	Ala	Val	Lys	Val		
			250					255					260				
TTT	TTT	ACC	ACT	GAA	GAA	GCT	AGC	TGG	TTT	AGA	GAA	ACA	GAA	ATC	TAC	1050	
Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr		
		265					270					275					
CAG	ACG	GTG	TTA	ATG	CGT	CAT	GAA	AAT	ATA	CTT	GGT	TTT	ATA	GCT	GCA	1098	
Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala		
		280				285					290						
GAC	ATT	AAA	GGC	ACT	GGT	TCC	TGG	ACT	CAG	CTG	TAT	TTG	ATT	ACT	GAT	1146	
Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp		
					300				305						310		
TAC	CAT	GAA	AAT	GGA	TCT	CTC	TAT	GAC	TTC	CTG	AAA	TGT	GCC	ACA	CTA	1194	

Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	Lys	Cys	Ala	Thr	Leu			
				315					320					325				
GAC	ACC	AGA	GCC	CTA	CTC	AAG	TTA	GCT	TAT	TCT	GCT	GCT	TGT	GGT	CTG	1242		
Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr	Ser	Ala	Ala	Cys	Gly	Leu			
				330					335					340				
TGC	CAC	CTC	CAC	ACA	GAA	ATT	TAT	GGT	ACC	CAA	GGG	AAG	CCT	GCA	ATT	1290		
Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile			
				345					350					355				
GCT	CAT	CGA	GAC	CTG	AAG	AGC	AAA	AAC	ATC	CTT	ATT	AAG	AAA	AAT	GGA	1338		
Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Ile	Lys	Lys	Asn	Gly			
				360					365					370				
AGT	TGC	TGT	ATT	GCT	GAC	CTG	GGC	CTA	GCT	GTT	AAA	TTC	AAC	AGT	GAT	1386		
Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Lys	Phe	Asn	Ser	Asp			
				375					380					385			390	
ACA	AAT	GAA	GTT	GAC	ATA	CCC	TTG	AAT	ACC	AGG	GTG	GGC	ACC	AAG	CGG	1434		
Thr	Asn	Glu	Val	Asp	Ile	Pro	Leu	Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg			
				395					400					405				
TAC	ATG	GCT	CCA	GAA	GTG	CTG	GAT	GAA	AGC	CTG	AAT	AAA	AAC	CAT	TTC	1482		
Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Ser	Leu	Asn	Lys	Asn	His	Phe			
				410					415					420				
CAG	CCC	TAC	ATC	ATG	GCT	GAC	ATC	TAT	AGC	TTT	GGT	TTG	ATC	ATT	TGG	1530		
Gln	Pro	Tyr	Ile	Met	Ala	Asp	Ile	Tyr	Ser	Phe	Gly	Leu	Ile	Ile	Trp			
				425					430					435				
GAA	ATG	GCT	CGT	CGT	TGT	ATT	ACA	GGA	GGA	ATC	GTG	GAG	GAA	TAT	CAA	1578		
Glu	Met	Ala	Arg	Arg	Cys	Ile	Thr	Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln			
				440					445					450				
TTA	CCA	TAT	TAC	AAC	ATG	GTG	CCC	AGT	GAC	CCA	TCC	TAT	GAG	GAC	ATG	1626		
Leu	Pro	Tyr	Tyr	Asn	Met	Val	Pro	Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met			
				455					460					465			470	
CGT	GAG	GTT	GTG	TGT	GTG	AAA	CGC	TTG	CGG	CCA	ATC	GTG	TCT	AAC	CGC	1674		
Arg	Glu	Val	Val	Cys	Val	Lys	Arg	Leu	Arg	Pro	Ile	Val	Ser	Asn	Arg			
				475					480					485				
TGG	AAC	AGC	GAT	GAA	TGT	CTT	CGA	GCA	GTT	TTG	AAG	CTA	ATG	TCA	GAA	1722		
Trp	Asn	Ser	Asp	Glu	Cys	Leu	Arg	Ala	Val	Leu	Lys	Leu	Met	Ser	Glu			
				490					495					500				
TGT	TGG	GCC	CAT	AAT	CCA	GCC	TCC	AGA	CTC	ACA	GCT	TTG	AGA	ATC	AAG	1770		
Cys	Trp	Ala	His	Asn	Pro	Ala	Ser	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys			
				505					510					515				
AAG	ACA	CTT	GCA	AAA	ATG	GTT	GAA	TCC	CAG	GAT	GTA	AAG	ATT			1812		
Lys	Thr	Leu	Ala	Lys	Met	Val	Glu	Ser	Gln	Asp	Val	Lys	Ile					
				520					525					530				
TGACAATTAA				ACAATTTTGA			GGGAGAATTT			AGACTGCAAG			AACTTCTTCA			CCCAAGGAAT		1872
GGGTGGGATT				AGCATGGAAT			AGGATGTTGA			CTTGGTTTCC			AGACTCCTTC			CTCTACATCT		1932
TCACAGGCTG				CTAACAGTAA			ACCTTACCGT			ACTCTACAGA			ATACAAG					

ACTTCAAACA TGTCATTCTT TATATATGAC AGCTTTGTTT TAATGTGGGG TTTTTTTGTT
 TGCTTTTTTT GTTTTGTT

2052

2070

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Thr	Gln	Leu	Tyr	Thr	Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Cys	Leu	Phe	1	5	10	15
Ile	Ile	Ser	His	Val	Gln	Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly	20	25	30	
Thr	Gly	Met	Lys	Ser	Asp	Leu	Asp	Gln	Lys	Lys	Pro	Glu	Asn	Gly	Val	35	40	45	
Thr	Leu	Ala	Pro	Glu	Asp	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser	50	55	60	
Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly	65	70	75	80
His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu	85	90	95	
Thr	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp	100	105	110	
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn	115	120	125	
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly	130	135	140	
Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Val	Leu	Ile	Ser	Met	145	150	155	160
Ala	Val	Cys	Ile	Val	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr	165	170	175	
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Gly	Arg	Tyr	Asn	Arg	Asp	180	185	190	
Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp	195	200	205	
Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu	210	215	220	
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val	225	230	235	240
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu	245	250	255	
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	260	265	270	
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	275	280	285	
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln	290	295	300	
Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe	305	310	315	320
Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr	325	330	335	
Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr	340	345	350	
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile				

TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC	192
Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly	
50 55 60	
GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT	240
Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro	
65 70 75	
GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA	288
Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr	
80 85 90	
CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC	336
His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro	
95 100 105	
AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC CCT GTG	384
Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val	
110 115 120 125	
GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC CTT ATC	432
Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile	
130 135 140	
ATT ATC ATC GTC TTC CTG GTC ATC AAC TAT CAC CAG CGT GTC TAC CAT	480
Ile Ile Ile Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His	
145 150 155	
AAC CGC CAG AGG TTG GAC ATG GAG GAC CCC TCT TGC GAG ATG TGT CTC	528
Asn Arg Gln Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu	
160 165 170	
TCC AAA GAC AAG ACG CTC CAG GAT CTC GTC TAC GAC CTC TCC ACG TCA	576
Ser Lys Asp Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser	
175 180 185	
GGG TCT GGC TCA GGG TTA CCC CTT TTT GTC CAG CGC ACA GTG GCC CGA	624
Gly Ser Gly Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg	
190 195 200 205	
ACC ATT GTT TTA CAA GAG ATT ATC GGC AAG GGC CGG TTC GGG GAA GTA	672
Thr Ile Val Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val	
210 215 220	
TGG CGT GGT CGC TGG AGG GGT GGT GAC GTG GCT GTG AAA ATC TTC TCT	720
Trp Arg Gly Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser	
225 230 235	
TCT CGT GAA GAA CGG TCT TGG TTC CGT GAA GCA GAG ATC TAC CAG ACC	768
Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr	
240 245 250	
GTC ATG CTG CGC CAT GAA AAC ATC CTT GGC TTT ATT GCT GCT GAC AAT	816
Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn	
255 260 265	
AAA GAT AAT GGC ACC TGG ACC CAG CTG TGG CTT GTC TCT GAC TAT CAC	864
Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His	
270 275 280 285	

GAG CAT GGC TCA CTG TTT GAT TAT CTG AAC CGC TAC ACA GTG ACC ATT	912
Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile	
290 295 300	
GAG GGA ATG ATT AAG CTA GCC TTG TCT GCA GCC AGT GGT TTG GCA CAC	960
Glu Gly Met Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His	
305 310 315	
CTG CAT ATG GAG ATT GTG GGC ACT CAA GGG AAG CCG GGA ATT GCT CAT	1008
Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His	
320 325 330	
CGA GAC TTG AAG TCA AAG AAC ATC CTG GTG AAA AAA AAT GGC ATG TGT	1056
Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys	
335 340 345	
GCC ATT GCA GAC CTG GGC CTG GCT GTC CGT CAT GAT GCG GTC ACT GAC	1104
Ala Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp	
350 355 360 365	
ACC ATA GAC ATT GCT CCA AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG	1152
Thr Ile Asp Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met	
370 375 380	
GCT CCT GAA GTC CTT GAC GAG ACA ATC AAC ATG AAG CAC TTT GAC TCC	1200
Ala Pro Glu Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser	
385 390 395	
TTC AAA TGT GCC GAC ATC TAT GCC CTC GGG CTT GTC TAC TGG GAG ATT	1248
Phe Lys Cys Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile	
400 405 410	
GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA CTG CCG	1296
Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro	
415 420 425	
TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG CGA AAG	1344
Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys	
430 435 440 445	
GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG TGG CAG	1392
Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln	
450 455 460	
AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG TGC TGG	1440
Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp	
465 470 475	
TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG AAG ACT	1488
Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr	
480 485 490	
CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT TAAGCTGTTC	1534
Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile	
495 500 505	
CTCTGCCTAC ACAAAGAACC TGGGCAGTGA GGATGACTGC AGCCACCGTG CAAGCGTCGT	1594
GGAGGCCTAT CCTCTTGTTT CTGCCCCGCC CTCTGGCAGA GCCCTGGCCT GCAAGAGGGA	1654

CAGAGCCTGG	GAGACGCGCG	CACTCCCGTT	GGGTTTGAGA	CAGACACTTT	TTATATTTAC	1714
CTCCTGATGG	CATGGAGACC	TGAGCAAATC	ATGTAGTCAC	TCAATGCCAC	AACTCAAAC	1774
GCTTCAGTGG	GAAGTACAGA	GACCCAGTGC	ATTGCGTGTG	CAGGAGCGTG	AGGTGCTGGG	1834
CTCGCCAGGA	GCGGCCCCCA	TACCTTGTGG	TCCACTGGGC	TGCAGGTTTT	CCTCCAGGGA	1894
CCAGTCAACT	GGCATCAAGA	TATTGAGAGG	AACCGGAAGT	TTCTCCCTCC	TTCCCGTAGC	1954
AGTCCTGAGC	CACACCATCC	TTCTCATGGA	CATCCGGAGG	ACTGCCCCTA	GAGACACAAC	2014
CTGCTGCCTG	TCTGTCCAGC	CAAGTGCGCA	TGTGCCGAGG	TGTGTCCCAC	ATTGTGCCTG	2074
GTCTGTGCCA	CGCCCGTGTG	TGTGTGTGTG	TGTGTGAGTG	AGTGTGTGTG	TGTACACTTA	2134
ACCTGCTTGA	GCTTCTGTGC	ATGTGT				2160

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met	Ala	Glu	Ser	Ala	Gly	Ala	Ser	Ser	Phe	Phe	Pro	Leu	Val	Val	Leu
1				5					10					15	
Leu	Leu	Ala	Gly	Ser	Gly	Gly	Ser	Gly	Pro	Arg	Gly	Ile	Gln	Ala	Leu
		20						25					30		
Leu	Cys	Ala	Cys	Thr	Ser	Cys	Leu	Gln	Thr	Asn	Tyr	Thr	Cys	Glu	Thr
		35					40					45			
Asp	Gly	Ala	Cys	Met	Val	Ser	Ile	Phe	Asn	Leu	Asp	Gly	Val	Glu	His
	50					55					60				
His	Val	Arg	Thr	Cys	Ile	Pro	Lys	Val	Glu	Leu	Val	Pro	Ala	Gly	Lys
	65				70					75					80
Pro	Phe	Tyr	Cys	Leu	Ser	Ser	Glu	Asp	Leu	Arg	Asn	Thr	His	Cys	Cys
			85						90					95	
Tyr	Ile	Asp	Phe	Cys	Asn	Lys	Ile	Asp	Leu	Arg	Val	Pro	Ser	Gly	His
		100						105					110		
Leu	Lys	Glu	Pro	Ala	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val
		115					120					125			
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile
	130					135					140				
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln
	145				150					155					160
Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp
			165						170					175	
Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly
		180						185					190		
Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val
		195					200					205			
Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly
	210					215					220				
Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu
	225				230					235				240	
Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu

TGGGAAGCGG CGGCGGGTTA ACTTCGGCTG AATCACAACC ATTTGGCGCT GAGCTATGAC	120
AAGAGAGCAA ACAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA GAAGTTTATT	180
GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys	228
1 5 10	
AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu	276
15 20 25 30	
CGT TGT AAA TGC CAC CAC CAC TGT CCG GAA GAC TCA GTC AAC AAT ATC Arg Cys Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile	324
35 40 45	
TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser	372
50 55 60	
GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp	420
65 70 75	
TTT CAA TGT CGT GAC ACT CCC ATT CCT CAT CAA AGA AGA TCA ATT GAA Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu	468
80 85 90	
TGC TGC ACA GAA AGG AAT GAG TGT AAT AAA GAC CTC CAC CCC ACT CTG Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu	516
95 100 105 110	
CCT CCT CTC AAG GAC AGA GAT TTT GTT GAT GGG CCC ATA CAC CAC AAG Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys	564
115 120 125	
GCC TTG CTT ATC TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile	612
130 135 140	
ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC CGA CCT CGG Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg	660
145 150 155	
TAC AGC ATT GGG CTG GAG CAG GAC GAG ACA TAC ATT CCT CCT GGA GAG Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu	708
160 165 170	
TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser	756
175 180 185 190	
GGC CTC CCT CTG CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met	804
195 200 205	
GTG AAG CAG ATT GGA AAA GGC CGC TAT GGC GAG GTG TGG ATG GGA AAG Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys	852
210 215 220	

TGG CGT GGA GAA AAG GTG GCT GTG AAA GTG TTC TTC ACC ACG GAG GAA	900
Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu	
225 230 235	
GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG CGG	948
Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg	
240 245 250	
CAT GAG AAT ATT CTG GGG TTC ATT GCT GCA GAT ATC AAA GGG ACT GGG	996
His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly	
255 260 265 270	
TCC TGG ACT CAG TTG TAC CTC ATC ACA GAC TAT CAT GAA AAC GGC TCC	1044
Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser	
275 280 285	
CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAC GCA AAG TCC ATG CTG	1092
Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu	
290 295 300	
AAG CTA GCC TAC TCC TCT GTC AGC GGC CTA TGC CAT TTA CAC ACG GAA	1140
Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu	
305 310 315	
ATC TTT AGC ACT CAA GGC AAG CCA GCA ATC GCC CAT CGA GAC TTG AAA	1188
Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys	
320 325 330	
AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC	1236
Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp	
335 340 345 350	
CTG GGC TTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATC	1284
Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile	
355 360 365	
CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG	1332
Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val	
370 375 380	
CTG GAC GAG AGC TTG AAT AGA AAC CAT TTC CAG TCC TAC ATT ATG GCT	1380
Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala	
385 390 395	
GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT	1428
Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys	
400 405 410	
GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCC TAT CAC GAC CTG	1476
Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu	
415 420 425 430	
GTG CCC AGT GAC CCT TCT TAT GAG GAC ATG AGA GAA ATT GTG TGC ATG	1524
Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met	
435 440 445	
AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT	1572
Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys	
450 455 460	

CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT	1620
Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro	
465 470 475	
GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG	1668
Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met	
480 485 490	
TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGTGGA CAGAGCAAGA	1722
Ser Glu Ser Gln Asp Ile Lys Leu	
495 500	
ATTTACACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCCC AGTGAGTTCA	1782
GACTTTCCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCAT	1842
CATGGCTTTC TGAGGAGGAG AAACGTGTTG GGTAACCTGT TCAAGATATG ATGCATGTTG	1902
CTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTTTT ATAAAAAAA	1952

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 502 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met	Leu	Leu	Arg	Ser	Ser	Gly	Lys	Leu	Asn	Val	Gly	Thr	Lys	Lys	Glu
1				5					10					15	
Asp	Gly	Glu	Ser	Thr	Ala	Pro	Thr	Pro	Arg	Pro	Lys	Ile	Leu	Arg	Cys
			20					25					30		
Lys	Cys	His	His	His	Cys	Pro	Glu	Asp	Ser	Val	Asn	Asn	Ile	Cys	Ser
		35					40					45			
Thr	Asp	Gly	Tyr	Cys	Phe	Thr	Met	Ile	Glu	Glu	Asp	Asp	Ser	Gly	Met
	50					55					60				
Pro	Val	Val	Thr	Ser	Gly	Cys	Leu	Gly	Leu	Glu	Gly	Ser	Asp	Phe	Gln
65					70				75					80	
Cys	Arg	Asp	Thr	Pro	Ile	Pro	His	Gln	Arg	Arg	Ser	Ile	Glu	Cys	Cys
				85				90						95	
Thr	Glu	Arg	Asn	Glu	Cys	Asn	Lys	Asp	Leu	His	Pro	Thr	Leu	Pro	Pro
			100					105					110		
Leu	Lys	Asp	Arg	Asp	Phe	Val	Asp	Gly	Pro	Ile	His	His	Lys	Ala	Leu
		115					120					125			
Leu	Ile	Ser	Val	Thr	Val	Cys	Ser	Leu	Leu	Leu	Val	Leu	Ile	Ile	Leu
	130					135					140				
Phe	Cys	Tyr	Phe	Arg	Tyr	Lys	Arg	Gln	Glu	Ala	Arg	Pro	Arg	Tyr	Ser
145					150				155					160	
Ile	Gly	Leu	Glu	Gln	Asp	Glu	Thr	Tyr	Ile	Pro	Pro	Gly	Glu	Ser	Leu
				165				170						175	

Arg	Asp	Leu	Ile	Glu	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu
			180					185					190		
Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Lys
		195					200					205			
Gln	Ile	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg
	210					215					220				
Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser
225					230					235				240	
Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu
				245					250					255	
Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp
		260						265					270		
Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr
	275						280					285			
Asp	Tyr	Leu	Lys	Ser	Thr	Thr	Leu	Asp	Ala	Lys	Ser	Met	Leu	Lys	Leu
	290					295					300				
Ala	Tyr	Ser	Ser	Val	Ser	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Phe
305					310					315				320	
Ser	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys
				325					330					335	
Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu	Gly
		340						345					350		
Leu	Ala	Val	Lys	Phe	Ile	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	Pro	Pro
	355						360					365			
Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Pro	Pro	Glu	Val	Leu	Asp
	370					375					380				
Glu	Ser	Leu	Asn	Arg	Asn	His	Phe	Gln	Ser	Tyr	Ile	Met	Ala	Asp	Met
385					390					395				400	
Tyr	Ser	Phe	Gly	Leu	Ile	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Cys	Val	Ser
			405						410					415	
Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	His	Asp	Leu	Val	Pro
		420						425					430		
Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met	Arg	Glu	Ile	Val	Cys	Met	Lys	Lys
	435						440					445			
Leu	Arg	Pro	Ser	Phe	Pro	Asn	Arg	Trp	Ser	Ser	Asp	Glu	Cys	Leu	Arg
	450					455					460				
Gln	Met	Gly	Lys	Leu	Met	Thr	Glu	Cys	Trp	Ala	Gln	Asn	Pro	Ala	Ser
465					470					475				480	
Arg	Leu	Thr	Ala	Leu	Arg	Val	Lys	Lys	Thr	Leu	Ala	Lys	Met	Ser	Glu
				485					490					495	
Ser	Gln	Asp	Ile	Lys	Leu										
			500												

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GCGGATCCTG TTGTGAAGGN AATATGTG

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GCGATCCGTC GCAGTCAAAA TTTT

24

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCGGATCCGC GATATATTAA AAGCAA

26

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CGGAATTCTG GTGCCATATA

20

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATTCAAGGGC ACATCAACTT CATTTGTGTC ACTGTTG

37

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GCGGATCCAC CATGGCGGAG TCGGCC

26

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AACACCGGGC CGGCGATGAT

20

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gly Xaa Gly Xaa Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Asp Phe Lys Ser Arg Asn
1 5

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Leu Lys Ser Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Gly Thr Lys Arg Tyr Met
1 5

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala Glu Val Tyr Lys Ala

				5					10					15			
Lys	Leu	Lys	Gln	Asn	Thr	Ser	Glu	Gln	Phe	Glu	Thr	Val	Ala	Val	Lys		
			20					25					30				
Ile	Phe	Pro	Tyr	Asp	His	Tyr	Ala	Ser	Trp	Lys	Asp	Arg	Lys	Asp	Ile		
		35					40					45					
Phe	Ser	Asp	Ile	Asn	Leu	Lys	His	Glu	Asn	Ile	Leu	Gln	Phe	Leu	Thr		
	50					55					60						
Ala	Glu	Glu	Arg	Lys	Thr	Glu	Leu	Gly	Lys	Gln	Tyr	Trp	Leu	Ile	Thr		
65					70					75					80		
Ala	Phe	His	Ala	Lys	Gly	Asn	Leu	Gln	Glu	Tyr	Leu	Thr	Arg	His	Val		
			85						90					95			
Ile	Ser	Trp	Glu	Asp	Leu	Arg	Asn	Val	Gly	Ser	Ser	Leu	Ala	Arg	Gly		
		100						105					110				
Leu	Ser	His	Leu	His	Ser	Asp	His	Thr	Pro	Cys	Gly	Arg	Pro	Lys	Met		
		115				120					125						
Pro	Ile	Val	His	Arg	Asp	Leu	Lys	Ser	Ser	Asn	Ile	Leu	Val	Lys	Asn		
	130					135					140						
Asp	Leu	Thr	Cys	Cys	Leu	Cys	Asp	Phe	Gly	Leu	Ser	Leu	Arg	Leu	Gly		
145					150					155					160		
Pro	Tyr	Ser	Ser	Val	Asp	Asp	Leu	Ala	Asn	Ser	Gly	Gln	Val	Gly	Thr		
			165						170					175			
Ala	Arg	Tyr	Met	Ala	Pro												
			180														

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Leu	Leu	Glu	Ile	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys	Ala		
			5						10					15			
Gln	Leu	Met	Asn	Asp	Phe	Val	Ala	Val	Lys	Ile	Phe	Pro	Leu	Gln	Asp		
		20						25				30					
Lys	Gln	Ser	Trp	Gln	Ser	Glu	Arg	Glu	Ile	Phe	Ser	Thr	Pro	Gly	Met		
		35				40					45						
Lys	His	Glu	Asn	Leu	Leu	Gln	Phe	Ile	Ala	Ala	Glu	Lys	Arg	Gly	Ser		
	50					55					60						
Asn	Leu	Glu	Val	Glu	Leu	Trp	Leu	Ile	Thr	Ala	Phe	His	Asp	Lys	Gly		
65					70					75					80		
Ser	Leu	Thr	Asp	Tyr	Leu	Lys	Gly	Asn	Ile	Ile	Thr	Trp	Asn	Glu	Leu		
			85					90					95				
Cys	His	Val	Ala	Glu	Thr	Met	Ser	Arg	Gly	Leu	Ser	Tyr	Leu	His	Glu		
		100						105					110				
Asp	Val	Pro	Trp	Cys	Arg	Gly	Glu	Gly	His	Lys	Pro	Ser	Ile	Ala	His		
		115				120					125						
Arg	Asp	Phe	Lys	Ser	Lys	Asn	Val	Leu	Leu	Lys	Ser	Asp	Leu	Thr	Ala		
	130					135					140						
Val	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Val	Arg	Phe	Glu	Pro	Gly	Lys	Pro		
145					150					155					160		
Pro	Gly	Asp	Thr	His	Gly	Gln	Val	Gly	Thr	Arg	Arg	Tyr	Met	Ala	Pro		
			165					170						175			

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Leu	Leu	Glu	Val	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys	Ala	
				5					10					15		
Gln	Leu	Leu	Asn	Glu	Tyr	Val	Ala	Val	Lys	Ile	Phe	Pro	Ile	Gln	Asp	
			20					25					30			
Lys	Gln	Ser	Trp	Gln	Asn	Glu	Tyr	Glu	Val	Tyr	Ser	Leu	Pro	Gly	Met	
			35				40					45				
Lys	His	Glu	Asn	Ile	Leu	Gln	Phe	Ile	Gly	Ala	Glu	Lys	Arg	Gly	Thr	
	50					55				60						
Ser	Val	Asp	Val	Asp	Leu	Trp	Leu	Ile	Thr	Ala	Phe	His	Glu	Lys	Gly	
65					70					75					80	
Ser	Leu	Ser	Asp	Phe	Leu	Lys	Ala	Asn	Val	Val	Ser	Trp	Asn	Glu	Leu	
				85					90					95		
Cys	His	Ile	Ala	Glu	Thr	Met	Ala	Arg	Gly	Leu	Ala	Tyr	Leu	His	Glu	
			100					105					110			
Asp	Ile	Pro	Gly	Leu	Lys	Asp	Gly	His	Lys	Pro	Ala	Ile	Ser	His	Arg	
			115				120					125				
Asp	Ile	Lys	Ser	Lys	Asn	Val	Leu	Leu	Lys	Asn	Asn	Leu	Thr	Ala	Cys	
	130					135					140					
Ile	Ala	Asp	Phe	Gly	Leu	Ala	Leu	Lys	Phe	Glu	Ala	Gly	Lys	Ser	Ala	
145					150					155					160	
Gly	Asp	Thr	His	Gly	Gln	Val	Gly	Thr	Arg	Arg	Tyr	Met	Ala	Pro		
				165				170						175		

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: C. elegans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Leu	Thr	Gly	Arg	Val	Gly	Ser	Gly	Arg	Phe	Gly	Asn	Val	Ser	Arg	Gly	
				5					10					15		
Asp	Tyr	Arg	Gly	Glu	Ala	Val	Ala	Val	Lys	Val	Phe	Asn	Ala	Leu	Asp	
			20					25					30			
Glu	Pro	Ala	Phe	His	Lys	Glu	Thr	Glu	Ile	Phe	Glu	Thr	Arg	Met	Leu	
			35				40					45				
Arg	His	Pro	Asn	Val	Leu	Arg	Tyr	Ile	Gly	Ser	Asp	Arg	Val	Asp	Thr	
	50					55					60					
Gly	Phe	Val	Thr	Glu	Leu	Trp	Leu	Val	Thr	Glu	Tyr	His	Pro	Ser	Gly	

65					70					75				80
Ser	Leu	His	Asp	Phe	Leu	Leu	Glu	Asn	Thr	Val	Asn	Ile	Glu	Thr
				85					90				95	
Tyr	Asn	Leu	Met	Arg	Ser	Thr	Ala	Ser	Gly	Leu	Ala	Phe	Leu	His
			100					105					110	
Gln	Ile	Gly	Gly	Ser	Lys	Glu	Ser	Asn	Lys	Pro	Ala	Met	Ala	His
		115				120						125		
Asp	Ile	Lys	Ser	Lys	Asn	Ile	Met	Val	Lys	Asn	Asp	Leu	Thr	Cys
	130					135					140			
Ile	Gly	Asp	Leu	Gly	Leu	Ser	Leu	Ser	Lys	Pro	Glu	Asp	Ala	Ala
145					150					155				160
Asp	Ile	Ile	Ala	Asn	Glu	Asn	Tyr	Lys	Cys	Gly	Thr	Val	Arg	Tyr
				165					170					175

Ala Pro

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 amino acids
- (B) TY7PE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MOUSE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Met	Gly	Ala	Ala	Ala	Lys	Leu	Ala	Phe	Ala	Val	Phe	Leu	Ile	Ser	Cys
				5					10					15	
Ser	Ser	Gly	Ala	Ile	Leu	Gly	Arg	Ser	Glu	Thr	Gln	Glu	Cys	Leu	Phe
		20					25						30		
Phe	Asn	Ala	Asn	Trp	Glu	lys	Asp	Arg	Thr	Asn	Gln	Thr	Gly	Val	Glu
	35						40					45			
Pro	Cys	Tyr	Gly	Asp	Lys	Asp	Lys	Arg	Arg	His	Cys	Phe	Ala	Thr	Trp
	50				55						60				
Lys	Asn	Ile	Ser	Gly	Ser	Ile	Glu	Ile	Val	Lys	Gln	Gly	Cys	Trp	Leu
65					70				75					80	
Asp	Asp	Ile	Asn	Cys	Tyr	Asp	Arg	Thr	Asp	Cys	Val	Glu	Lys	Lys	Asp
			85						90					95	
Ser	Pro	Glu	Val	Tyr	Phe	Cys	Cys	Cys	Glu	Gly	Asn	Met	Cys	Asn	Glu
		100						105					110		
Lys	Phe	Ser	Tyr	Phe	Pro	Glu	Met	Glu	Val	Thr	Gln	Pro	Thr	Ser	Asn
	115						120					125			
Pro	Val	Thr	Pro	Lys	Pro	Pro	Tyr	Tyr	Asn	Ile	Leu	Leu	Tyr	Ser	Leu
	130					135					140				
Val	Pro	Leu	Met	Leu	Ile	Ala	Gly	Ile	Val	Ile	Cys	Ala	Phe	Trp	Val
145					150				155						160
Tyr	Arg	His	His	Lys	Met	Ala	Tyr	Pro	Pro	Val	Leu	Val	Pro	Thr	Gln
				165					170					175	
Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu	Leu	Gly	Leu	Lys	Pro	Leu
		180					185						190		
Gln	Leu	Leu	Glu	Val	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys
	195						200					205			
Ala	Gln	Leu	Leu	Asn	Glu	Tyr	Val	Ala	Val	Lys	Ile	Phe	Pro	Ile	Gln
	210					215					220				
Asp	Lys	Gln	Ser	Trp	Gln	Asn	Glu	Tyr	Glu	Val	Tyr	Ser	Leu	Pro	Gly

225		230		235		240
Met	Lys	His	Glu	Asn	Ile	Leu
				245		
Thr	Ser	Val	Asp	Val	Asp	Leu
				260		
Gly	Ser	Leu	Ser	Asp	Phe	Leu
				275		
Leu	Cys	His	Ile	Ala	Glu	Thr
				290		
Glu	Asp	Ile	Pro	Gly	Leu	Lys
305				310		
Arg	Asp	Ile	Lys	Ser	Lys	Asn
				325		
Cys	Ile	Ala	Asp	Phe	Gly	Leu
				340		
Ala	Gly	Asp	Thr	His	Gly	Gln
				355		
Glu	Val	Leu	Glu	Gly	Ala	Ile
370				375		
Ile	Asp	Met	Tyr	Ala	Met	Gly
385				390		
Cys	Thr	Ala	Ala	Asp	Gly	Pro
				405		
Glu	Glu	Ile	Gly	Gln	His	Pro
				420		
Val	His	Lys	Lys	Lys	Arg	Pro
				435		
Ala	Gly	Met	Ala	Met	Leu	Cys
450				455		
Asp	Ala	Glu	Ala	Arg	Leu	Ser
465				470		
Gln	Met	Gln	Arg	Leu	Thr	Asn
				485		
Val	Val	Thr	Met	Val	Thr	Asn
				500		
Leu						

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: MOUSE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Met	Thr	Ala	Pro	Trp	Ala	Ala	Leu	Ala	Leu	Leu	Trp	Gly	Ser	Leu	Cys
				5					10					15	
Ala	Gly	Ser	Gly	Arg	Gly	Glu	Ala	Glu	Thr	Arg	Glu	Cys	Ile	Tyr	Tyr
			20				25					30			
Asn	Ala	Asn	Trp	Glu	Leu	Glu	Arg	Thr	Asn	Gln	Ser	Gly	Leu	Glu	Arg
		35				40					45				
Cys	Glu	Gly	Glu	Gln	Asp	Lys	Arg	Leu	His	Cys	Tyr	Ala	Ser	Trp	Arg

50	Asn	Ser	Ser	Gly	Thr	Ile	Glu	Leu	Val	Lys	Lys	Gly	Cys	Trp	Leu	Asp
65	Asp	Phe	Asn	Cys	Tyr	Asp	Arg	Gln	Glu	Cys	Val	Ala	Thr	Glu	Glu	Asn
				85						90					95	
	Pro	Gln	Val	Tyr	Phe	Cys	Cys	Cys	Glu	Gly	Asn	Phe	Cys	Asn	Glu	Arg
				100					105					110		
	Phe	Thr	His	Leu	Pro	Glu	Pro	Gly	Gly	Pro	Glu	Val	Thr	Tyr	Glu	Pro
			115					120					125			
	Pro	Pro	Thr	Ala	Pro	Thr	Leu	Leu	Thr	Val	Leu	Ala	Tyr	Ser	Leu	Leu
			130				135					140				
	Pro	Ile	Gly	Gly	Leu	Ser	Leu	Ile	Val	Leu	Leu	Ala	Phe	Trp	Met	Tyr
145						150					155					160
	Arg	His	Arg	Lys	Pro	Pro	Tyr	Gly	His	Val	Asp	Ile	His	Glu	Val	Arg
				165						170					175	
	Gln	Cys	Gln	Arg	Trp	Ala	Gly	Arg	Arg	Asp	Gly	Cys	Ala	Asp	Ser	Phe
				180				185						190		
	Lys	Pro	Leu	Pro	Phe	Gln	Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu
			195				200						205			
	Val	Gly	Leu	Lys	Pro	Leu	Gln	Leu	Leu	Glu	Ile	Lys	Ala	Arg	Gly	Arg
			210				215					220				
	Phe	Gly	Cys	Val	Trp	Lys	Ala	Gln	Leu	Met	Asn	Asp	Phe	Val	Ala	Val
225						230					235					240
	Lys	Ile	Phe	Pro	Leu	Gln	Asp	Lys	Gln	Ser	Trp	Gln	Ser	Glu	Arg	Glu
				245						250					255	
	Ile	Phe	Ser	Thr	Pro	Gly	Met	Lys	His	Glu	Asn	Leu	Leu	Gln	Phe	Ile
				260			265							270		
	Ala	Ala	Glu	Lys	Arg	Gly	Ser	Asn	Leu	Glu	Val	Glu	Leu	Trp	Leu	Ile
			275				280						285			
	Thr	Ala	Phe	His	Asp	Lys	Gly	Ser	Leu	Thr	Asp	Tyr	Leu	Lys	Gly	Asn
			290				295					300				
	Ile	Ile	Thr	Trp	Asn	Glu	Leu	Cys	His	Val	Ala	Glu	Thr	Met	Ser	Arg
305					310						315					320
	Gly	Leu	Ser	Tyr	Leu	His	Glu	Asp	Val	Pro	Trp	Cys	Arg	Gly	Glu	Gly
				325						330					335	
	His	Lys	Pro	Ser	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Lys	Asn	Val	Leu
			340					345						350		
	Leu	Lys	Ser	Asp	Leu	Thr	Ala	Val	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Val
			355				360						365			
	Arg	Phe	Glu	Pro	Gly	Lys	Pro	Pro	Gly	Asp	Thr	His	Gly	Gln	Val	Gly
			370				375					380				
	Thr	Arg	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe
385						390					395					400
	Gln	Arg	Asp	Ala	Phe	Leu	Arg	Ile	Asp	Met	Tyr	Ala	Met	Gly	Leu	Val
				405					410						415	
	Leu	Trp	Glu	Leu	Val	Ser	Arg	Cys	Lys	Ala	Ala	Asp	Gly	Pro	Val	Asp
			420					425						430		
	Glu	Tyr	Met	Leu	Pro	Phe	Glu	Glu	Glu	Ile	Gly	Gln	His	Pro	Ser	Leu
			435				440						445			
	Glu	Glu	Leu	Gln	Glu	Val	Val	Val	His	Lys	Lys	Met	Arg	Pro	Thr	Ile
			450				455					460				
	Lys	Asp	His	Trp	Leu	Lys	His	Pro	Gly	Leu	Ala	Gln	Leu	Cys	Val	Thr
465					470						475					480
	Ile	Glu	Glu	Cys	Trp	Asp	His	Asp	Ala	Glu	Ala	Arg	Leu	Ser	Ala	Gly
				485					490						495	
	Cys	Val	Glu	Glu	Arg	Val	Ser	Leu	Ile	Arg	Arg	Ser	Val	Asn	Gly	Thr
			500					505					510			
	Thr	Ser	Asp	Cys	Leu	Val	Ser	Leu	Val	Thr	Ser	Val	Thr	Asn	Val	Asp
			515					520					525			
	Leu	Leu	Pro	Lys	Glu	Ser	Ser	Ile								

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu
      5              10              15
Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val
      20              25              30
Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro
      35              40              45
Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln
      50              55              60
Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro
      65              70              75              80
Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr
      85              90              95
Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile
      100             105             110
Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys
      115             120             125
Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn
      130             135             140
Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu
      145             150             155             160
Leu Leu Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu
      165             170             175
Gly Val Ala Ile Ser Val Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn
      180             185             190
Arg Gln Gln Lys Leu Ser Ser Thr Trp Glu Thr Gly Lys Thr Arg Lys
      195             200             205
Leu Met Glu Phe Ser Glu His Cys Ala Ile Ile Leu Glu Asp Asp Arg
      210             215             220
Ser Asp Ile Ser Ser Thr Cys Ala Asn Asn Ile Asn His Asn Thr Glu
      225             230             235             240
Leu Leu Pro Ile Glu Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala
      245             250             255
Glu Val Tyr Lys Ala Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu
      260             265             270
Thr Val Ala Val Lys Ile Phe Pro Tyr Glu Glu Tyr Ala Ser Trp Lys
      275             280             285
Thr Glu Lys Asp Ile Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile
      290             295             300
Leu Gln Phe Leu Thr Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln
      305             310             315             320
Tyr Trp Leu Ile Thr Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr
      325             330             335
Leu Thr Arg His Val Ile Ser Trp Glu Asp Leu Arg Lys Leu Gly Ser
      340             345             350

```


(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Asp Leu Lys Pro Glu Asn

5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Asp Leu Ala Ala Arg Asn

5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Asp Ile Lys Ser Lys Asn

5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Asp Phe Lys Ser Lys Asn

5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Asp Leu Lys Ser Ser Asn
5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: First Xaa is Thr or Ser;
fourth Xaa is Tyr or Phe; Each other Xaa
may be any amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Gly Xaa Xaa Xaa Xaa Xaa
5

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: Fisrt Xaa is any amino acid;
second Xaa is Ile or Val;
third Xaa is Lys or Arg;
fourth Xaa is Thr or Met.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Xaa Pro Xaa Xaa Trp Xaa
5

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Gly Thr Arg Arg Tyr Met

5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Gly Thr Ala Arg Tyr Met

5

*See
E3
included
D1
cont*